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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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10/728,509

12/05/2003

Hong Zhang

ISPH-0803

9823

55389 7590 01/03/2008  
KNOBBE, MARTENS, OLSON & BEAR, LLP  
2040 MAIN STREET  
FOURTEENTH FLOOR  
IRVINE, CA 92614

EXAMINER

ZARA, JANE J

ART UNIT

PAPER NUMBER

1635

MAIL DATE

DELIVERY MODE

01/03/2008

PAPER

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

## Office Action Summary

Application No.

10/728,509

Applicant(s)

ZHANG ET AL.

Examiner

Jane Zara

Art Unit

1635

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

### Status

- 1) ☒ Responsive to communication(s) filed on 16 November 2007.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

### Disposition of Claims

- 4) ☒ Claim(s) 1-9 and 11-18 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-9 and 11-18 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

### Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

### Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO/SB/08)  
Paper No(s)/Mail Date \_\_\_\_\_
- 4) ☐ Interview Summary (PTO-413)  
Paper No(s)/Mail Date. \_\_\_\_\_
- 5) ☐ Notice of Informal Patent Application
- 6) ☒ Other: Sequence Alignment Data



### **DETAILED ACTION**

This Office action is in response to the communication filed 11-16-07.

Claims 1-9, 11-18 are pending in the instant application.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

### ***Election/Restrictions***

SEQ ID Nos. other than SEQ ID No. 64 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected invention, there being no allowable generic or linking claim. Election was made **without** traverse in the reply filed on 11-16-07.

Applicant's election without traverse of SEQ ID No. 64 in the reply filed on 11-16-07 is acknowledged.

### ***Response to Arguments and Amendments***

#### **Withdrawn Rejections**

Any rejections not repeated in this Office action are hereby withdrawn.

#### **Rejections Necessitated by Amendments**

#### ***Claim Rejections - 35 USC § 112***

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-9, 11-18 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

In claim 1, line 2, it is unclear whether the recited phrase "12 linked nucleosides" refers to contiguously linked nucleobases, or non-contiguous nucleobases. Appropriate clarification is required.

Claims 15 and 16 recite compounds comprising or consisting of "any of" a single sequence. The metes and bounds of the claimed invention cannot be determined. Appropriate correction is required.

It is unclear whether the description of "each internucleoside linkage is a phosphorothioate linkage" (last line of claim 18) refers to the entire oligonucleotide, or the gap or wing segments only. Appropriate clarification is required.

### ***Claim Rejections - 35 USC § 102/103***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all

obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 1-3, 7, 11, and 13-15 are rejected under 35 U.S.C. 102(e) as being anticipated by or, in the alternative, under 35 U.S.C. 103(a) as obvious over Mittman et al (USPN 6,821,724).

Mittman et al (USPN 6,821,724) teach compositions and methods of inhibiting a known target gene of interest comprising administering an antisense oligonucleotide between 12-30 nucleobases in length comprising at least 12 linked nucleosides of SEQ ID No. 64, a pharmaceutically acceptable diluent, and which oligonucleotide optionally further comprises modified nucleobases and internucleotide linkages(see SEQ ID No. 2494 of Mittman et al, see also col. 1-2 and 4, claim 1; see also the accompanying sequence alignment data). The burden of establishing whether the prior art oligonucleotide has the function of inhibiting gene expression as claimed falls to applicant. See (In re Best, 562 F.2d 1252, 1255, 195 USPQ 430, 433-434 (CCPA 1977): "Where, as here, the claimed and prior art products are identical or substantially identical, or are produced by identical or substantially identical processes, the PTO can require an applicant to prove that the prior art products do not necessarily or inherently possess the characteristics of his claimed product... Whether the rejection is based on 'inherency' under 35 USC 102, on 'prima facie obviousness' under 35 USC 103, jointly or alternatively, the burden of proof is the same, and its fairness is evidenced b the PTO's inability to manufacture products or to obtain and compare prior art products

[footnote omitted]." See also MPEP 2112: "[T]he PTO can require an applicant to prove that the prior art products do not necessarily or inherently possess the characteristics of his [her] claimed product." The MPEP at 2112 citing *In re Fitzgerald* 205 USPQ 594, 596 (CCPA 1980), quoting *In re Best* 195 USPQ 430 as per above. Therefore, absent evidence to the contrary, since the oligonucleotides disclosed by Zhou et al meet all of the structural limitations of the instantly claimed invention, it would necessarily be presumed to have the functionality claimed, of specifically inhibiting expression of BCL2-associated x protein in vitro.

Therefore, absent evidence to the contrary, claims 1, 2, 10, 11, and 13 are anticipated by or, in the alternative, obvious over Mittman et al.

### ***Claim Rejections - 35 USC § 103***

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 1-9, 11-18 are rejected under 35 U.S.C. 103(a) as being unpatentable over Mittman et al (USPN 6,821,724) as applied to claims 1-3, 7, 11, and 13-15 above, in view of Korsmeyer (USPN 6,500,626) and further in view of Milner et al and McKay insofar as the claims are drawn to compositions and methods of inhibiting the expression of the BCL2-associated x protein in vitro comprising administration of a

composition comprising an antisense oligonucleotide between 12-30 nucleobases in length comprising at least 12 linked nucleosides of nucleobases of SEQ ID NO: 64, which oligonucleotide comprises a phosphorothioate internucleotide linkage, a 2'-O-methoxyethyl sugar moiety and a 5'-methyl-cytosine, and which is optionally a chimeric oligonucleotide, and which composition further comprises a colloidal dispersion system and gap segment consisting of ten linked deoxynucleotides, a 5' wing segment consisting of five linked nucleotides, a 3' wing segment consisting of five linked nucleotides, and which gap segment is between the 5' and 3' wings, and each wing comprises a 2'-O-methoxyethyl sugar and wherein each internucleoside linkage is a phosphorothioate linkage.

Mittman et al (USPN 6,821,724) is relied upon as cited in the 102/103 rejection above.

Mittman does not teach antisense oligonucleotides comprising phosphorothioate internucleotide linkages, 2'-O-methoxyethyl modified sugar moieties or 5-methyl cytosine nucleobases, nor chimeric antisense oligonucleotides, nor colloidal dispersion systems, gapmers.

Korsmeyer (6,500,626) teach the inhibition of expression of SEQ ID No. 17, encoding the BCL2-associated x protein, using antisense oligonucleotides (see col. 29 and col. 46, lines 54-56).

Milner et al (Nature Biotech. 15: 537-541, 1997) teach methods of designing and testing antisense oligonucleotides for their ability to specifically hybridize and inhibit the expression of a target nucleic acid of known nucleotide sequence in vitro, including in

the 5', 3' and stop codon regions of the target gene (See figure 1 on p 538 and figures 5-7 on pages 539-540).

McKay et al (USPN 6,133,246, 10-17-00) teach colloidal dispersion compositions comprising antisense oligonucleotides between 12 and 30 nucleobases in length which optionally comprise modified internucleotide linkages including phosphorothioate linkages, modified nucleobases including 5-methylcytosine, modified sugar moieties including 2'-O-methoxyethyl sugars, and wherein the antisense is optionally a chimeric oligonucleotide, and antisense oligonucleotides optionally design choices of modifications comprising 5' wing segments consisting of five linked nucleotides, 3' wing segments consisting of five linked nucleotides, and a gap segment between the 5' and 3' wings, wherein each wing comprises a 2'-O-methoxyethyl sugar and wherein each internucleoside linkage is a phosphorothioate linkage, and which antisense targets various regions of a target gene. McKay et al also teach the in vitro inhibition and screening of modulators (e.g. of various antisense oligonucleotides between 12-30 nucleobases that specifically hybridize with the target gene).

It would have been obvious to one of ordinary skill in the art to design and utilize antisense oligonucleotides between 12-20 nucleobases in length comprising at least 12 contiguous nucleobases of SEQ ID NO. 64 to inhibit the expression of SEQ ID No. 17, encoding the BCL2-associated x protein (BAX) in vitro, because Mittman teaches this antisense sequence, and Milner et al and McKay teach the ability to design and assess antisense oligonucleotides for their ability to inhibit the expression of a target gene of known nucleotide sequence in vitro, including various regions of the target gene of

interest, using routine screening assays that are well known in the art (see Milner at pages 539-540 and McKay at col. 6-15). It would have been obvious to one of ordinary skill in the art to target and inhibit the expression of BCL2-associated x protein in vitro comprising the administration of antisense oligonucleotides between 12-30 nucleobases because Mittman teaches such antisense sequences for targeting and inhibiting the expression of a known target gene, Milner teaches methods of designing and assessing antisense oligonucleotides between 8-50 nucleobases for their ability to target and inhibit the expression of a known target gene in vitro. One of ordinary skill in the art would have been motivated to utilize such a method of finding optimal antisense oligonucleotides between 12-30 nucleobases which best target and inhibit BCL2-associated x protein expression in order to study this target molecule's role in apoptosis, and its role in pathologies related to aberrant expression of BAX, including such conditions as Parkinson's, Alzheimer's.

One of ordinary skill in the art would have expected that the methods of designing and assessing antisense oligonucleotides for inhibiting a target gene of known sequence, which were taught by Milner et al, and also taught by McKay to be routine for a previously characterized target gene, would successfully be used to identify numerous antisense oligonucleotides (between 12-30 nucleobases) for the in vitro inhibition of BCL2-associated x protein expression. One of ordinary skill in the art would have been motivated to incorporate the nucleobase, internucleotide linkage and sugar modifications, as well as chimeric structures, into antisense oligonucleotides because such modifications (including 5-methyl cytosine, 2'-O-methoxyethyl and

phosphorothioate linkages) have been taught previously by McKay et al to increase target binding, cellular uptake and antisense stability. One of ordinary skill in the art would have expected that the delivery of modified antisense oligonucleotides to target cells harboring BCL2-associated x protein, which antisense specifically hybridize with the target nucleic acid encoding BCL2-associated x protein (e.g. of the 3' UTR of SEQ ID No. 17), would lead to inhibition of expression of BCL2-associated x protein in vitro.

Therefore, the invention as a whole would have obvious to one of ordinary skill in the art at the time the invention was made.

### ***Conclusion***

**THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Certain papers related to this application may be submitted to Art Unit 1635 by facsimile transmission. The faxing of such papers must conform with the notices



Application/Control Number:  
10/728,509  
Art Unit: 1635

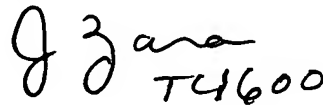
Page 10

published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 C.F.R. ' 1.6(d)). The official fax telephone number for the Group is 571-273-8300. NOTE: If Applicant does submit a paper by fax, the original signed copy should be retained by applicant or applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jane Zara whose telephone number is (571) 272-0765. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, James Douglas Schultz, can be reached on (571) 272-0763. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Jane Zara  
12-26-07

Handwritten signature of Jane Zara in cursive script, with the initials 'TZ' and the number '600' written below it.

JANE ZARA, PH.D.  
PRIMARY EXAMINER

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Scientific and Technical Information Center

SEARCH REQUEST FORM

CRFE

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 11-30-07  
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 101728,509  
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: AS MODN of BCL-2 Assoc.  
Inventors (please provide full names): H. Zhang et al

Earliest Priority Date: 12-8-03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No 64  
① - oligo search - limit to 50 NTS.  
② { Score over length 70 - 100% IDents.  
size range 12 - 30 Nucleotides.

please include Antisense Searches

Thanks

64-20na  
LB

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Type of Search

Vendors and cost where applicable

Searcher: \_\_\_\_\_

\_\_\_\_\_ NA Sequence (#)

\_\_\_\_\_ STN \_\_\_\_\_ Dialog

Searcher Phone #: \_\_\_\_\_

\_\_\_\_\_ AA Sequence (#)

\_\_\_\_\_ Questel/Orbit \_\_\_\_\_ Lexis/Nexis

Searcher Location: \_\_\_\_\_

\_\_\_\_\_ Structure (#)

\_\_\_\_\_ Westlaw \_\_\_\_\_ WWW/Internet

Date Searcher Picked Up: \_\_\_\_\_

\_\_\_\_\_ Bibliographic

\_\_\_\_\_ In-house sequence systems

Date Completed: \_\_\_\_\_

\_\_\_\_\_ Litigation

\_\_\_\_\_ Commercial \_\_\_\_\_ Oligomer \_\_\_\_\_ Score/Length  
\_\_\_\_\_ Interference \_\_\_\_\_ SPDI \_\_\_\_\_ Encode/Transl  
\_\_\_\_\_ Other (specify)

Searcher Prep & Review Time: \_\_\_\_\_

\_\_\_\_\_ Fulltext

Online Time: \_\_\_\_\_

\_\_\_\_\_ Other

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RESULT 4
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; Sequence 157899, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 157899
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-157899

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 1165052, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1165052
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1165052

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Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCC 18
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RESULT 6
US-10-310-914B-1175079/c
; Sequence 1175079, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
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Sequence  
Alignment  
DATA

PLEASE SCAN  
EMAIL

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; SEQ ID NO 1175079
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1175079

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Qy 1 GCCCCAGTTGAAG 13
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RESULT 7
US-09-396-196G-2494/c
; Sequence 2494, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2494
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-2494

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RESULT 8
US-10-719-900-62297/c
; Sequence 62297, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719.900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 62297
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-62297

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:12:43 ; Search time 935 Seconds

(without alignments)  
80.129 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

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Scoring table:

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Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 10: /EMC\_Celerra\_SIDS2/ptodata/1/ina/RE COMB.seq.\*
- 11: /EMC\_Celerra\_SIDS2/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	14	70.0	37	5	US-09-060-299-146
4	13	65.0	20	6	US-10-310-914B-157899
5	13	65.0	20	6	US-10-310-914B-1165052
6	13	65.0	23	6	US-10-310-914B-1175079
7	13	65.0	25	3	US-09-396-196G-2494
8	13	65.0	25	5	US-10-719-900-62297
9	13	65.0	25	5	US-10-719-900-76493
10	13	65.0	25	5	US-10-719-900-168653
11	13	65.0	25	5	US-10-719-900-311855
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13	13	65.0	25	5	US-10-719-900-975477
14	13	65.0	50	3	US-10-131-827-5954
15	13	65.0	50	3	US-10-131-827-6319
16	13	65.0	50	5	US-10-131-831-5954
17	13	65.0	50	5	US-10-131-831-6319
18	13	65.0	50	5	US-10-325-899-5954
19	13	65.0	50	5	US-10-325-899-5954
20	12	60.0	15	3	US-08-584-040-8471
21	12	60.0	15	3	US-09-371-772B-4126
22	12	60.0	15	3	US-09-685-664B-4126

c 23	12	60.0	15	5	US-10-138-674B-4126	Sequence 4126, Ap
c 24	12	60.0	17	3	US-08-584-040-3879	Sequence 3879, Ap
c 25	12	60.0	17	3	US-08-584-040-3880	Sequence 3880, Ap
c 26	12	60.0	17	3	US-09-371-772B-1646	Sequence 1646, Ap
c 27	12	60.0	17	3	US-09-371-772B-1647	Sequence 1647, Ap
c 28	12	60.0	17	3	US-09-371-772B-6253	Sequence 6253, Ap
c 29	12	60.0	17	3	US-09-371-772B-6254	Sequence 6254, Ap
c 30	12	60.0	17	3	US-09-685-664B-1646	Sequence 1646, Ap
c 31	12	60.0	17	3	US-09-685-664B-1647	Sequence 1647, Ap
c 32	12	60.0	17	5	US-10-138-674B-1646	Sequence 1646, Ap
c 33	12	60.0	17	5	US-10-138-674B-1647	Sequence 1647, Ap
c 34	12	60.0	17	5	US-10-138-674B-6253	Sequence 6253, Ap
c 35	12	60.0	17	5	US-10-138-674B-6254	Sequence 6254, Ap
c 36	12	60.0	17	5	US-10-138-674B-8571	Sequence 8571, Ap
c 37	12	60.0	19	6	US-10-310-914B-1191074	Sequence 1191074, Ap
c 38	12	60.0	25	3	US-08-997-685A-30	Sequence 30, Appl
c 39	12	60.0	25	3	US-09-086-436-18	Sequence 18, Appl
c 40	12	60.0	25	5	US-10-719-900-113603	Sequence 113603, Ap
c 41	12	60.0	25	5	US-10-719-900-464231	Sequence 464231, Ap
c 42	12	60.0	25	5	US-10-719-900-582537	Sequence 582537, Ap
c 43	12	60.0	25	5	US-10-719-900-632716	Sequence 632716, Ap
c 44	12	60.0	25	5	US-10-719-900-657676	Sequence 657676, Ap
c 45	12	60.0	25	5	US-10-719-900-731099	Sequence 731099, Ap

## ALIGNMENTS

RESULT 1  
US-09-060-299-146  
; Sequence 146, Application US/09060299  
; Patent No. 6545137  
; GENERAL INFORMATION:  
; APPLICANT: Todd, John A  
; APPLICANT: Hess, John W  
; APPLICANT: Caskey, Charles T  
; APPLICANT: Cox, Roger D  
; APPLICANT: Gerhold, David  
; APPLICANT: Hammond, Holly  
; APPLICANT: Hey, Patricia  
; APPLICANT: Kawaguchi, Yoshihiko  
; APPLICANT: Merriman, Tony R  
; APPLICANT: Metzker, Michael L  
; TITLE OF INVENTION: No. 6545137el Receptor  
; NUMBER OF SEQUENCES: 455  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Nixon and Vanderhye  
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: US  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/060,299  
; FILING DATE: 15-APR-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043,553  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/048,740  
; FILING DATE: 05-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: B.J.Sadoff  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 620-35  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4091  
; TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-060-299-146

Query Match 70.0%; Score 14; DB 3; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17  
|||||  
DB 14 CCAGTTGAAGTTGC 27

#### RESULT 2

US-09-402-923A-146

; Sequence 146, Application US/09402923A

; Patent No. 6555654

GENERAL INFORMATION:

APPLICANT: Todd, John A

Hess, John W

Caskey, Charles T

Cox, Roger D

Gerhold, David

Hammond, Holly

Hey, Patricia

Kawaguchi, Yoshihiko

Merriman, Tony R

Metzker, Michael L

TITLE OF INVENTION: No. 6555654e1 LDL-Receptor

NUMBER OF SEQUENCES: 455

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon and Vanderhye

STREET: 1100 No. 6555654th Glebe Road, Eighth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: US

ZIP: VA 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,923A

FILING DATE: 14-Feb-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01102

FILING DATE: 15-APR-1998

APPLICATION NUMBER: US 60/043,553

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 60/048,740

FILING DATE: 05-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: B.J.Sadoff

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 620-81

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4091

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 146:

US-09-402-923A-146

Query Match

70.0%; Score 14; DB 3; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17  
|||||  
DB 14 CCAGTTGAAGTTGC 27

#### RESULT 3

US-10-331-907-146

; Sequence 146, Application US/10331907

; Patent No. 7244577

GENERAL INFORMATION:

APPLICANT: Todd, John A

Hess, John W

Caskey, Charles T

Cox, Roger D

Gerhold, David

Hammond, Holly

Hey, Patricia

Kawaguchi, Yoshihiko

Merriman, Tony R

Metzker, Michael L

TITLE OF INVENTION: No. 7244577e1 LDL-Receptor

NUMBER OF SEQUENCES: 455

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon and Vanderhye

STREET: 1100 No. 7244577th Glebe Road, Eighth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: US

ZIP: VA 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/331,907

FILING DATE: 31-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,923A

FILING DATE: 14-Feb-2001

APPLICATION NUMBER: PCT/GB98/01102

FILING DATE: 15-APR-1998

APPLICATION NUMBER: US 60/043,553

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 60/048,740

FILING DATE: 05-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: B.J.Sadoff

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 620-81

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4091

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 146:

US-10-331-907-146

Query Match 70.0%; Score 14; DB 5; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17  
|||||  
DB 14 CCAGTTGAAGTTGC 27

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RESULT 4
US-10-910-914B-157899/c
; Sequence 157899, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 157899
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-157899

Query Match      65.0%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
      |||||
Db      14 AGTTGAAGTTGCC 2

RESULT 5
US-10-310-914B-1165052
; Sequence 1165052, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1165052
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1165052

Query Match      65.0%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
      |||||
Db      14 AGTTGAAGTTGCC 2

RESULT 6
US-10-310-914B-1175079/c
; Sequence 1175079, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1175079
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1175079

Query Match      65.0%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCCAGTTGAAG 13
      |||||
Db      21 GCCCAGTTGAAG 9
```

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; SEQ ID NO 1175079
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1175079

Query Match      65.0%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCCAGTTGAAG 13
      |||||
Db      21 GCCCAGTTGAAG 9

RESULT 7
US-09-396-196G-2494/c
; Sequence 2494, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2494
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-2494

Query Match      65.0%; Score 13; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTGCCG 19
      |||||
Db      17 GTTGAAGTTGCCG 5

RESULT 8
US-10-719-900-62297/c
; Sequence 62297, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 62297
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-62297

Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
```

```
Db      16 AGTTGAAGTTGCC 4
|||||
RESULT 9
US-10-719-900-76493
; Sequence 76493, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 76493
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-76493
Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CCCAGTTGAAGT 14
|||||
Db      9 CCCAGTTGAAGT 21
|||||

RESULT 10
US-10-719-900-168653/c
; Sequence 168653, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 168653
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-168653
Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTGCC 18
|||||
Db      18 AGTTGAAGTTGCC 6
|||||

RESULT 11
US-10-719-900-311855
; Sequence 311855, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 311855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-311855
Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 CCCAGTTGAAGTT 15
|||||
Db      8 CCCAGTTGAAGTT 20
|||||

RESULT 12
US-10-719-900-974745/c
; Sequence 974745, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 974745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-974745
Query Match      65.0%; Score 13; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTGCC 18
|||||
Db      22 AGTTGAAGTTGCC 10
|||||

RESULT 13
US-10-719-900-975477/c
; Sequence 975477, Application US/10719900
; Patent No. 7250289
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; Patent No. 7250289
; SEQ ID NO 975477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-975477
Query Match      65.0%; Score 13; DB 5; Length 25;
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Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19  
Db 20 GTTGAAGTTGCCG 8

RESULT 14

US-10-131-827-5954/c  
; Sequence 5954, Application US/10131827  
; Patent No. 6905827  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5954  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-5954

Query Match 65.0%; Score 13; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCC 18  
Db 14 AGTTGAAGTTGCC 2

RESULT 15

US-10-131-827-6319/c  
; Sequence 6319, Application US/10131827  
; Patent No. 6905827  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6319  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-6319

Query Match 65.0%; Score 13; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCC 18  
Db 14 AGTTGAAGTTGCC 2

Search completed: December 3, 2007, 16:28:20  
Job time : 937 secs



GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model  
Run on: December 3, 2007, 15:56:26 ; Search time 12284 Seconds  
(without alignments)  
133.279 Million cell updates/sec

Title: US-10-728-509-64  
Perfect score: 20  
Sequence: 1 gccccagttgaagttgccgt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 9588671 seqs, 4092980300 residues

Word size : 1

Total number of hits satisfying chosen parameters: 3986186

Minimum DB seq length: 0  
Maximum DB seq length: 50

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- 7: gb\_srs.\*
- 8: gb\_sy.\*
- 9: gb\_un.\*
- 10: gb\_vi.\*
- 11: gb\_ov.\*
- 12: gb\_in.\*
- 13: gb\_om.\*
- 14: gb\_ba.\*
- 15: gb\_htgl.\*
- 16: gb\_htg2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	16	80.0	20	2	DD248708	DD248708 Screening
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4	16	80.0	20	2	DD404058	DD404058 Method of
c	5	14	70.0	25	CS174774	CS174774 Sequence
6	14	70.0	37	2	BD106103	BD106103 Novel LDL
7	14	70.0	37	2	AR305192	AR305192 Sequence
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ALIGNMENTS

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DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis accelerator and an apoptosis inhibitor.  
ACCESSION DD236265  
VERSION DD236265.1 GI:94046395  
KEYWORDS WO 2005093082-A/16.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Nakagawara,A. and Ozaki,T.  
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis accelerator and an apoptosis inhibitor  
JOURNAL Patent: WO 2005093082-A 16 06-OCT-2005;  
COMMENT Hisamitsu Pharmaceutical Co Inc  
OS Artificial  
PN WO 2005093082-A/16  
PD 06-OCT-2005  
PF 23-MAR-2005 WO 2005JP005247  
PR 14-JUN-2004 JP 200 4-176107,26-MAR-2004 JP 200 4-093266 PI  
akira nakagawara.toshifumi ozaki  
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LOCUS DD248708 20 bp DNA linear PAT 18-MAY-2006
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis accelerator and an apoptosis inhibitor.
ACCESSION DD248708
VERSION DD248708.1 GI:99024603
KEYWORDS JP 2005304470-A/16.
SOURCE unclassified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakagawara,A. and Ozaki,T.
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis accelerator and an apoptosis inhibitor
JOURNAL Patent: JP 2005304470-A 16 04-NOV-2005,
Hisamitsu Pharmaceutical Co Inc
COMMENT OS Artificial
PN JP 2005304470-A/16
PD 04-NOV-2005
PF 14-JUN-2004 JP 2004176107
PI akira nakagawara,toshifumi ozaki
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DB 1 CAGTTGAAGTTGCCGT 16
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LOCUS DD402954 20 bp DNA linear PAT 21-FEB-2007
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis inhibitor.
ACCESSION DD402954
VERSION DD402954.1 GI:126146805
KEYWORDS JP 2006223265-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakagawara,A. and Ozaki,T.
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic
compounds, an apoptosis inhibitor
JOURNAL Patent: JP 2006223265-A 8 31-AUG-2006;
Hisamitsu Pharmaceutical Co Inc
COMMENT OS Homo sapiens
PN JP 2006223265-A/8
PD 31-AUG-2006
PF 21-FEB-2005 JP 2005044554
PI akira nakagawara,toshifumi ozaki
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DB 1 CAGTTGAAGTTGCCGT 16
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DD404058
LOCUS DD404058 20 bp DNA linear PAT 21-FEB-2007
DEFINITION Method of screening a gene related to a quantity of HCV.
ACCESSION DD404058
VERSION DD404058.1 GI:126149401
KEYWORDS WO 2006085407-A/21.
SOURCE unclassified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baumi,M. and Takayama,T.
TITLE Method of screening a gene related to a quantity of HCV
JOURNAL Patent: WO 2006085407-A 21 17-AUG-2006;
Nihon University
COMMENT OS Artificial
PN WO 2006085407-A/21
PD 17-AUG-2006
PF 30-SEP-2005 WO 2005JP018573
PR 09-FEB-2005 JP 05P 033707
PI mariko esumi,tadatoshi takayama
CC primer
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DB 1 CAGTTGAAGTTGCCGT 16
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LOCUS CS174774 25 bp DNA linear PAT 14-JUL-2006
DEFINITION Sequence 13 from Patent WO2005090394.
ACCESSION CS174774
VERSION CS174774.1 GI:77625627
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Oswald,S., Weckbecker,C., Huthmacher,K., Gerasimova,T.,
Novikov,A., Ryabchenko,L., Yankenko,A. and Egorova,K.
TITLE Cyanide tolerant nitrilhydratases
JOURNAL Patent: WO 2005090394-A 13 29-SEP-2005;
DEGUSSA AG (DE)
FH Key Location/Qualifiers.
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DEFINITION
ACCESSION  BD106103
VERSION     BD106103.1 GI:23200921
KEYWORDS   JP 2002501376-A/118.
SOURCE     Chlamydia sp.
ORGANISM   Bacteria; Chlamydiae; Chlamydiaceae; Chlamydia.
REFERENCE  1 (bases 1 to 37)
AUTHORS    Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H.
and Hey,P.
TITLE      Novel LDL-receptor
JOURNAL    Patent: JP 2002501376-A 118 15-JAN-2002;
THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
INC
COMMENT    PN JP 2002501376-A/118
PD 15-JAN-2002
PF 15-APR-1998 JP 1998543635
PR 15-APR-1997 US 60/043553.05-JUN-1997 US 60/048740 PI
JOHN ANDREW TODD,JOHN WILFRED HESS,CHARLES
THOMAS CASKEY,ROGER
PI DAVID COX,
PI DAVID GERHOLD,HOLLY HAMMOND,PATRICIA HEY
PC C12N15/12,C12N15/11,C12Q1/68,C07K14/705,C07K16/28,A61K38/17,
PC A61K39/395,
PC A61K48/00
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CC Topology: Linear;
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LOCUS      AR305192
DEFINITION  Sequence 146 from patent US 6545137.
ACCESSION  AR305192
VERSION     AR305192.1 GI:31694502
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 37)
AUTHORS    Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L., Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
Receptor
TITLE      Receptor
JOURNAL    Patent: US 6545137-A 146 08-APR-2003;
Location/Qualifiers
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RESULT 8
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LOCUS      AR309296
DEFINITION  Sequence 146 from patent US 6555654.
ACCESSION  AR309296
VERSION     AR309296.1 GI:31701301
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 37)
AUTHORS    Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L., Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
LDL-receptor
TITLE      LDL-receptor
JOURNAL    Patent: US 6555654-A 146 29-APR-2003;
The Wellcome Trust Limited as Trustee for the Wellcome Trust;
London;
WOX;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17
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DEFINITION  Sequence 146 from patent US 7244577.
ACCESSION  EA268023
VERSION     EA268023.1 GI:155713612
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 37)
AUTHORS    Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L., Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
Method of screening for modulator of LRP5 activity
TITLE      Method of screening for modulator of LRP5 activity
JOURNAL    Patent: US 7244577-A 146 17-JUL-2007;
Merck & Co., Inc.; Rahway, NJ;
US;
Location/Qualifiers
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DEFINITION  Sequence 146 from patent US 7244577.
ACCESSION  EA268023
VERSION     EA268023.1 GI:155713612
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 37)
AUTHORS    Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L., Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
Method of screening for modulator of LRP5 activity
TITLE      Method of screening for modulator of LRP5 activity
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Merck & Co., Inc.; Rahway, NJ;
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LOCUS AX488224 20 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 5524 from Patent WO02053728.  
ACCESSION AX488224  
VERSION AX488224.1 GI:22322304  
KEYWORDS  
SOURCE Candida albicans  
ORGANISM Candida albicans  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Mitosporic Saccharomycetales; Candida.

REFERENCE 1  
Roemer, T., Jiang, B., Boone, C., Buesey, H. and Ohlsen, K.L.  
TITLE Gene disruption methodologies for drug target discovery  
JOURNAL Patent: WO 02053728-A 5524 11-JUL-2002;  
Eli Lilly Pharmaceuticals, Inc. (US)

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QY 7 GTTGAAGTTGCCG 19  
Db 17 GTTGAAGTTGCCG 5

RESULT 11  
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LOCUS EA258028 50 bp DNA linear PAT 14-AUG-2007  
DEFINITION Sequence 5954 from patent US 7235358.  
ACCESSION EA258028  
VERSION EA258028.1 GI:155699406  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Wohlgenuth, J., Fry, K., Woodward, R., Ly, N. and Prentice, J.  
TITLE Methods and compositions for diagnosing and monitoring transplant rejection  
JOURNAL Patent: US 7235358-A 5954 26-JUN-2007;  
Expression Diagnostics, Inc.; South San Francisco, CA;  
US;

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QY 6 AGTTGAAGTTGCC 18  
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RESULT 12  
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LOCUS EA258393 50 bp DNA linear PAT 14-AUG-2007  
DEFINITION Sequence 6319 from patent US 7235358.  
ACCESSION EA258393  
VERSION EA258393.1 GI:155699771  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Wohlgenuth, J., Fry, K., Woodward, R., Ly, N. and Prentice, J.  
TITLE Methods and compositions for diagnosing and monitoring transplant rejection  
JOURNAL Patent: US 7235358-A 6319 26-JUN-2007;  
Expression Diagnostics, Inc.; South San Francisco, CA;  
US;

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LOCUS AR686890 50 bp DNA linear PAT 12-SEP-2005  
DEFINITION Sequence 6319 from patent US 6905827.  
ACCESSION AR686890  
VERSION AR686890.1 GI:74468660  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)

AUTHORS Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.  
TITLE Methods and compositions for diagnosing or monitoring auto immune  
and chronic inflammatory diseases  
JOURNAL Patent: US 6905827-A 6319 14-JUN-2005;  
Expression Diagnostics, Inc.; So. San Francisco, CA  
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DEFINITION Sequence 5954 from patent US 7026121.  
ACCESSION AR827293  
VERSION AR827293.1 GI:111851108  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 50)  
AUTHORS Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.  
TITLE Methods and compositions for diagnosing and monitoring transplant  
rejection  
JOURNAL Patent: US 7026121-A 5954 11-APR-2006;  
Expression Diagnostics, Inc.; South San Francisco, CA;  
US;  
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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 20

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Post-processing: Minimum Score over Length 70%  
Listing first 1000 summaries

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16: gb\_htg2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Score		Query		Match		Length		DB		ID		Description	
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C 33	8.8	73.3	44.0	12	2	AX098969	Se
C 34	8.8	73.3	44.0	12	2	AX136994	Se
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C 38	10	71.4	50.0	14	2	A88710	Sequ
C 39	10	71.4	50.0	14	2	AR774929	Se
C 40	12	70.6	60.0	17	2	CS508144	Se
C 41	12	70.6	60.0	17	2	DD126995	NU
C 42	12	70.6	60.0	17	2	AR188391	Se
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C 44	12	70.6	60.0	17	2	AR324244	Se
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C 47	12	70.6	60.0	17	2	AR328852	Se
C 48	12	70.6	60.0	17	2	AR328853	Se
C 49	12	70.6	60.0	17	2	AR597704	Se
C 50	12	70.6	60.0	17	2	AR597705	Se
C 51	12	70.6	60.0	17	2	AR841343	Se
C 52	12	70.6	60.0	17	2	AR841344	Se
C 53	12	70.6	60.0	17	2	AR845950	Se
C 54	12	70.6	60.0	17	2	AR845951	Se
C 55	12	70.6	60.0	17	2	AR848268	Se
C 56	8.4	70.0	42.0	12	2	AR101078	Se
C 57	8.4	70.0	42.0	12	2	CS097732	Se
C 58	8.4	70.0	42.0	12	2	CS097756	Se
C 59	8.4	70.0	42.0	12	2	CS540753	Se
C 60	8.4	70.0	42.0	12	2	I07921	Sequ
C 61	8.4	70.0	42.0	12	2	I34823	Sequ
C 62	8.4	70.0	42.0	12	2	AR893297	Se
C 63	8.4	70.0	42.0	12	2	AR893306	Se

## ALIGNMENTS

RESULT 1	BD066222	14 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD066222	An antisense oligonucleotide preparation method.			
DEFINITION	BD066222	An antisense oligonucleotide preparation method.			
ACCESSION	BD066222				
VERSION	BD066222.1	GI:22611825			
KEYWORDS	JP 2001511000-A/857.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	1 (bases 1 to 14)				
AUTHORS	Schlingensiefen, K.H. and Brysch, W.				
TITLE	An antisense oligonucleotide preparation method				
JOURNAL	Patent: JP 2001511000-A 857 07-AUG-2001;				
COMMENT	BIOGENOSIT GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH				
	OS Unknown				
	PN JP 2001511000-A/857				
	PD 07-AUG-2001				
	PF 30-JAN-1998 JP 1998532533				
	PP 31-JAN-1997 EP 97101531.8				
	PR KARL HERMANN SCHLINGENSIEFEN, WOLFGANG BRYSCH				
	PC C12N15/11, C07H21/04, A61K13/70				
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LOCUS A42517 14 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 33 from Patent WO9502051.
ACCESSION A42517
VERSION A42517.1 GI:2297966
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and Brysch,W.
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL Patent: WO 9502051-A 33 19-JAN-1995;
COMMENT BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
Other publication AU 7345694 950206.
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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2 GTTGAAGTTGCTG 14

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LOCUS A88709 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 857 from Patent WO9833904.
ACCESSION A88709
VERSION A88709.1 GI:6737279
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 857 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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DEFINITION Sequence 857 from patent US 6972171.
ACCESSION AR774928
VERSION AR774928.1 GI:83352192
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.-H. and Brysch,W.
TITLE Antisense oligonucleotide preparation method
JOURNAL Patent: US 6972171-A 857 06-DEC-2005;
BIOGNOSTIK Ges. fur biomolekulare diagnostik mbH; Gottingen; EPX;
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DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis accelerator and an apoptosis inhibitor.
ACCESSION DD236265
VERSION DD236265.1 GI:94046395
KEYWORDS WO 2005093082-A/16.
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakagawara,A. and Ozaki,T.
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis accelerator and an apoptosis inhibitor
JOURNAL Patent: WO 2005093082-A 16 06-OCT-2005;
Hisamitsu Pharmaceutical Co Inc
COMMENT OS Artificial
PN WO 2005093082-A/16
PD 06-OCT-2005
PF 23-MAR-2005 WO 2005JP005247
PR 14-JUN-2004 JP 200 4-176107,26-MAR-2004 JP 200 4-093266 PI
akira nakagawara, toshifumi ozaki
CC primer for Bax
FH Key Location/Qualifiers
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DD248708 20 bp DNA linear PAT 18-MAY-2006  
LOCUS  
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis accelerator and an apoptosis inhibitor.  
DD248708  
ACCESSION  
VERSION DD248708.1 GI:99024603  
KEYWORDS JP 2005304470-A/16.  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Nakagawara,A. and Ozaki,T.  
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis accelerator and an apoptosis inhibitor  
JOURNAL Patent: JP 2005304470-A 16 04-NOV-2005;  
COMMENT Hisamitsu Pharmaceutical Co Inc  
PN JP 2005304470-A/16  
PD 04-JUN-2005  
PI akira nakagawara,toshifumi ozaki  
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RESULT 7  
DD402954 20 bp DNA linear PAT 21-FEB-2007  
LOCUS  
DEFINITION Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis inhibitor.  
DD402954  
ACCESSION  
VERSION DD402954.1 GI:126146805  
KEYWORDS JP 2006223265-A/8.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 20)  
TITLE Screening methods for pro-apoptotic compounds or anti-apoptotic compounds, an apoptosis accelerator and an apoptosis inhibitor.  
JOURNAL Patent: JP 2006223265-A 8 31-AUG-2006;  
COMMENT Hisamitsu Pharmaceutical Co Inc  
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PI akira nakagawara,toshifumi ozaki  
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DD404058 20 bp DNA linear PAT 21-FEB-2007  
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DEFINITION Method of screening a gene related to a quantity of HCV.  
DD404058  
ACCESSION  
VERSION DD404058.1 GI:126149401  
KEYWORDS WO 2006085407-A/21.  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Esami,M. and Takayama,T.  
TITLE Method of screening a gene related to a quantity of HCV  
JOURNAL Patent: WO 2006085407-A 21 17-AUG-2006;  
COMMENT Nihon University  
PN WO 2006085407-A/21  
PD 17-AUG-2006  
PI 30-SEP-2005 WO 2005JP018573  
PR 09-FEB-2005 JP 05P 033707  
PI mariko esumi,tadatoshi takayama  
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ACCESSION  
VERSION AR192983.1 GI:20238948



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ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 15)
AUTHORS      Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6346398-A 8471 12-FEB-2002;
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RESULT 10
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DEFINITION Sequence 4126 from patent US 6566127.
ACCESSION  AR326724
VERSION     AR326724.1 GI:33712532
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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
              Patent: US 6566127-A 4126 20-MAY-2003;
JOURNAL     Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
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DEFINITION Sequence 4126 from patent US 6818447.
ACCESSION  AR600184
VERSION     AR600184.1 GI:56651198
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
              Patent: US 6818447-A 4126 16-NOV-2004;
JOURNAL     Sirna Therapeutics, Inc.; Boulder, CO

KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 15)
AUTHORS      Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
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JOURNAL      Patent: US 6346398-A 8471 12-FEB-2002;
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ACCESSION  AR843823
VERSION     AR843823.1 GI:111931376
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ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Enzymatic nucleic acid-mediated treatment of ocular diseases or
              conditions related to levels of vascular endothelial growth factor
              receptor (VEGF-R)
              Patent: US 7034009-A 4126 25-APR-2006;
JOURNAL     Sirna Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
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RESULT 13
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DEFINITION USING POLYAMIDE NUCLEIC ACID OLIGOMERS TO ENGENDER A BIOLOGICAL
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ACCESSION  BD376104
VERSION     BD376104.1 GI:92275004
KEYWORDS    JP 2003523307-A/14.
SOURCE      Rattus sp.
ORGANISM    Rattus sp.
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              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Jansen,K., Hoshall,C.V., Tyler,B.M., McCormick,D.J., Cusack,B.M.,
              Douglas,C.L. and Richelson,E.
TITLE       USING POLYAMIDE NUCLEIC ACID OLIGOMERS TO ENGENDER A BIOLOGICAL
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JOURNAL     Patent: JP 2003523307-A 14 05-AUG-2003;
              MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH
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PF 16-OCT-1998 JP 2000516984  
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08-OCT-1998 US 09/168714,30-JAN-1998 US 09/016685, PR  
PI karen jansen,clark v hoshall,beth marie tyler,daniel j PI  
mccormick,  
PI bernadette marie cusack,christopher lee douglas,elliott PI  
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DEFINITION Sequence 14 from patent US 6723560.  
ACCESSION AR527594  
VERSION AR527594.1 GI:53914707  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Richelson,E., Tyler,B.M., Cusack,B.M., Douglas,C.L. and Jansen,K.  
TITLE Using polyamide nucleic acid oligomers to engender a biological response  
JOURNAL Patent: US 6723560-A 14 20-APR-2004;  
Mayo Foundation for Medical Education and Research; Rochester, MN  
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LOCUS 14 bp DNA linear PAT 05-APR-2006  
DEFINITION Sequence 14 from patent US 6989270.  
ACCESSION AR791253  
VERSION AR791253.1 GI:91138201  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Richelson,E., Tyler,B.M., Cusack,B.M., Douglas,C.L. and Jansen,K.  
TITLE Using polyamide nucleic acid oligomers to engender a biological response  
PF 16-OCT-1998 JP 2000516984  
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PI karen jansen,clark v hoshall,beth marie tyler,daniel j PI  
mccormick,  
PI bernadette marie cusack,christopher lee douglas,elliott PI  
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DEFINITION Sequence 14 from patent US 6723560.  
ACCESSION AR527594  
VERSION AR527594.1 GI:53914707  
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REFERENCE 1 (bases 1 to 14)  
AUTHORS Richelson,E., Tyler,B.M., Cusack,B.M., Douglas,C.L. and Jansen,K.  
TITLE Using polyamide nucleic acid oligomers to engender a biological response  
JOURNAL Patent: US 6723560-A 14 20-APR-2004;  
Mayo Foundation for Medical Education and Research; Rochester, MN  
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TITLE Using polyamide nucleic acid oligomers to engender a biological response  
JOURNAL Patent: US 6989270-A 14 24-JAN-2006;  
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AR328405  
LOCUS 16 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 5807 from patent US 6566127.  
ACCESSION AR328405  
VERSION AR328405.1 GI:33714213  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 5807 20-MAY-2003;  
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
source Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned RNA"  
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Query Match 59.0%; Score 11.8; DB 2; Length 16;  
Score over Length 73.8%;  
Best Local Similarity 86.7%; Pred. No. 1.9e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCCCCAGTTGAAGTTT 15  
|  
Db 2 GACCCAGATGAAGTTT 16  
RESULT 17  
AR845504  
LOCUS 16 bp RNA linear PAT 10-AUG-2006  
DEFINITION Sequence 5807 from patent US 7034009.  
ACCESSION AR845504  
VERSION AR845504.1 GI:111933057  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or conditions related to levels of vascular endothelial growth factor receptor (VEGF-R)  
JOURNAL Patent: US 7034009-A 5807 25-APR-2006;  
Sirta Therapeutics, Inc. and Chiron Corporation; Boulder, CO;  
US;  
FEATURES  
source Location/Qualifiers  
1. .16  
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/mol\_type="unassigned RNA"

## ORIGIN

Query Match 59.0%; Score 11.8; DB 2; Length 16;  
 Score over Length 73.3%;  
 Best Local Similarity 86.7%; Pred. No. 1.9e+05;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15  
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 Db 2 GACCCAGATGAAGTT 16

RESULT 18  
 BD209027/c  
 LOCUS 15 bp RNA linear PAT 04-NOV-2005  
 DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.  
 ACCESSION BD209027  
 VERSION BD209027.1 GI:33018797  
 KEYWORDS JP 2002512791-A/2617.  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified sequences.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Blatt, L., McSwiggen, J. A., Roberts, E., Pavco, P. A. and Macejak, D.  
 TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection  
 JOURNAL Patent: JP 2002512791-A 2617 08-MAY-2002;  
 COMMENT RIBOZYME PHARMACEUTICALS INC  
 OS Hepatitis virus (hepatitis C virus)  
 PN JP 2002512791-A/2617  
 PD 08-MAY-2002  
 PF 26-APR-1999 JP 2000545991  
 PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR  
 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI  
 LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI  
 PAVCO,  
 PI DENNIS MACEJAK  
 PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,  
 PC A61K37/66,  
 PC C12N15/00  
 CC Enzymatic nucleic acid treatment of diseases or conditions related to  
 CC hepatitis C virus infection.  
 FH Key Location/Qualifiers  
 FT source 1. .15  
 FT virus). Location/Qualifiers

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source  
 1. .15  
 /organism="unidentified"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32644"

## ORIGIN

Query Match 55.0%; Score 11; DB 2; Length 15;  
 Score over Length 73.3%;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGAAG 13  
 | | | | | | | | | | | | |  
 Db 15 CCAGTTGAAGT 5

## RESULT 19

AR193008/c  
 LOCUS 15 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 8496 from patent US 6346398.  
 ACCESSION AR193008  
 VERSION AR193008.1 GI:20238973  
 KEYWORDS  
 SOURCE Unknown.

## ORGANISM

Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
 JOURNAL Patent: US 6346398-A 8496 12-FEB-2002;  
 FEATURES Location/Qualifiers  
 source 1. .15  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 55.0%; Score 11; DB 2; Length 15;  
 Score over Length 73.3%;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
 | | | | | | | | | | | | |  
 Db 15 CCAGTTGAAGT 5

RESULT 20  
 AR326748/c  
 LOCUS 15 bp RNA linear PAT 17-AUG-2003  
 DEFINITION Sequence 4150 from patent US 6566127.  
 ACCESSION AR326748  
 VERSION AR326748.1 GI:33712556  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Pavco, P., McSwiggen, J. A., Stinchcomb, D. T. and Escobedo, J.  
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
 JOURNAL Patent: US 6566127-A 4150 20-MAY-2003;  
 FEATURES Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
 Location/Qualifiers  
 source 1. .15  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

## ORIGIN

Query Match 55.0%; Score 11; DB 2; Length 15;  
 Score over Length 73.3%;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
 | | | | | | | | | | | | |  
 Db 15 CCAGTTGAAGT 5

## RESULT 21

AR600208/c  
 LOCUS 15 bp RNA linear PAT 15-DEC-2004  
 DEFINITION Sequence 4150 from patent US 6818447.  
 ACCESSION AR600208  
 VERSION AR600208.1 GI:56651222  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
 JOURNAL Patent: US 6818447-A 4150 16-NOV-2004;  
 FEATURES Sirna Therapeutics, Inc.; Boulder, CO  
 Location/Qualifiers  
 source 1. .15

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/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match      55.0%; Score 11; DB 2; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14
    |||||
Db 15 CCAGTTGAAGT 5

RESULT 22
AR843847/c
LOCUS AR843847 15 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 4150 from patent US 7034009.
ACCESSION AR843847
VERSION AR843847.1 GI:111931400
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 4150 25-APR-2006;
        Sirna Therapeutics, Inc. and Chiron Corporation, Boulder, CO;
        US;
FEATURES
    source      Location/Qualifiers
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    /mol_type="unassigned RNA"

ORIGIN
Query Match      55.0%; Score 11; DB 2; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14
    |||||
Db 15 CCAGTTGAAGT 5

RESULT 23
BD211445
LOCUS BD211445 12 bp DNA linear PAT 04-NOV-2005
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
ACCESSION BD211445
VERSION BD211445.1 GI:33021215
KEYWORDS JP 2002510492-A/14.
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Ford,J. and Pace,A.
TITLE A novel interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: JP 2002510492-A 14 09-APR-2002;
        HYSEQ INC
COMMENT OS Artificial Sequence
        PN JP 2002510492-A/14
        PD 09-APR-2002
        PR 05-APR-1999 JP 2000542457
        PR 03-APR-1998 US 09/055010.15-MAY-1998 US 09/079909 PR
        20-MAY-1998 US 09/082364.19-JUN-1998 US 09/099818 PR
        31-JUL-1998 US 09/127698.13-JAN-1999 US 09/229591 PR
        17-FEB-1999 US 09/251370
        PI JOHN FORD, ANN PACE
        PC C12N15/09,A61K38/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,

PC C12N1/19,
PC C12N1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/566,G01N33/68, PC
C12N15/00,
PC A61K37/02,C12N5/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..12
    /organism='Artificial Sequence'.
FEATURES
    source      Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"

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Query Match      44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
    |||||
Db 1 CCACAGTGAAG 12

RESULT 24
AR058661
LOCUS AR058661 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 238 from patent US 5837832.
ACCESSION AR058661
VERSION AR058661.1 GI:5984238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
        Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 238 17-NOV-1998;
        Location/Qualifiers
FEATURES
    source      Location/Qualifiers
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    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
Query Match      44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
    |||||
Db 1 TGGAGTTGCAGT 12

RESULT 25
AR058662
LOCUS AR058662 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 239 from patent US 5837832.
ACCESSION AR058662
VERSION AR058662.1 GI:5984239
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
        Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 239 17-NOV-1998;
        Location/Qualifiers
FEATURES
    source      Location/Qualifiers
    1..12
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Db 1 CCACAGGTGAAG 12

RESULT 28  
AR221139  
LOCUS AR221139 12 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 22 from patent US 6426191.  
ACCESSION AR221139  
VERSION AR221139.1 GI:23328024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Ford, J. and Pace, A.  
TITLE Assays involving an IL-1 receptor antagonist  
JOURNAL Patent: US 6426191-A 22 30-JUL-2002;  
Hysq, Inc.; Sunnyvale, CA  
FEATURES  
source  
1..12  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 44.0%; Score 8.8; DB 2; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.2e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13  
|||||  
Db 1 CCACAGGTGAAG 12

RESULT 29  
AR302967  
LOCUS AR302967 12 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 22 from patent US 6541623.  
ACCESSION AR302967  
VERSION AR302967.1 GI:31691567  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Ford, J., Ho, A.S.Y. and Pace, A.  
TITLE Interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: US 6541623-A 22 01-APR-2003;  
Hysq, Inc.; Sunnyvale, CA  
FEATURES  
source  
1..12  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 44.0%; Score 8.8; DB 2; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.2e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13  
|||||  
Db 1 CCACAGGTGAAG 12

RESULT 30  
AR948135  
LOCUS AR948135 12 bp DNA linear PAT 08-OCT-2006  
DEFINITION Sequence 357 from patent US 7115364.  
ACCESSION AR948135  
VERSION AR948135.1 GI:115839540  
KEYWORDS  
SOURCE Unknown.

Db 1 CCACAGGTGAAG 12

RESULT 26  
EA008497  
LOCUS EA008497 12 bp DNA linear PAT 06-DEC-2006  
DEFINITION Sequence 32 from patent US 7122652.  
ACCESSION EA008497  
VERSION EA008497.1 GI:118817729  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Wojnowski, L. and Hustert, E.  
TITLE Polymorphisms in the human hpxr gene and their use diagnostic and  
therapeutic applications  
JOURNAL Patent: US 7122652-A 32 17-OCT-2006;  
source  
1..12  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 44.0%; Score 8.8; DB 2; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.2e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13  
|||||  
Db 1 CCACAGGTGAAG 12

RESULT 27  
AR182005  
LOCUS AR182005 12 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 22 from patent US 6337072.  
ACCESSION AR182005  
VERSION AR182005.1 GI:20224921  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Ford, J. and Pace, A.  
TITLE Interleukin-1 receptor antagonist and recombinant production  
JOURNAL Patent: US 6337072-A 22 08-JAN-2002;  
source  
1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 44.0%; Score 8.8; DB 2; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.2e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13  
|||||

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Chee, M., Cronin, M.T., Fodor, S.P.A., Gingeras, T.R., Huang, X.C., Hubbell, E.A., Lipshutz, R.J., Lobb, P.E., Miyada, C.G., Morris, M.S., Shah, N. and Sheldan, E.L.  
TITLE Arrays of nucleic acid probes on biological chips  
JOURNAL Patent: US 7115364-A 357 03-OCT-2006; Affymetrix, Inc.; Santa Clara, CA; US;

FEATURES  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 44.0%; Score 8.8; DB 2; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.2e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCGT 20  
Db 1 TGGAGTTGAGT 12

RESULT 31  
LOCUS AR948136 12 bp DNA linear PAT 08-OCT-2006  
DEFINITION Sequence 358 from patent US 7115364.  
ACCESSION AR948136  
VERSION AR948136.1 GI:115839541  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Chee, M., Cronin, M.T., Fodor, S.P.A., Gingeras, T.R., Huang, X.C., Hubbell, E.A., Lipshutz, R.J., Lobb, P.E., Miyada, C.G., Morris, M.S., Shah, N. and Sheldan, E.L.  
TITLE Arrays of nucleic acid probes on biological chips  
JOURNAL Patent: US 7115364-A 358 03-OCT-2006; Affymetrix, Inc.; Santa Clara, CA; US;

FEATURES  
source Location/Qualifiers  
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/mol\_type="genomic DNA"

ORIGIN  
Query Match 44.0%; Score 8.8; DB 2; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.2e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17  
Db 1 ATTTGAGTTGC 12

RESULT 32  
LOCUS AX069325 12 bp DNA linear PAT 25-JAN-2001  
DEFINITION Sequence 22 from Patent WO0102571.  
ACCESSION AX069325  
VERSION AX069325.1 GI:12579191  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Ford, J. and Pace, A.  
TITLE A interleukin-1 receptor antagonist and uses thereof

JOURNAL Patent: WO 0102571-A 22 11-JAN-2001;  
HYSEQ, INC. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Splice Acceptor Site"

ORIGIN  
Query Match 44.0%; Score 8.8; DB 2; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.2e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13  
Db 1 CCACAGGTGAAG 12

RESULT 33  
LOCUS AX098969 12 bp DNA linear PAT 02-APR-2001  
DEFINITION Sequence 32 from Patent WO0120026.  
ACCESSION AX098969  
VERSION AX098969.1 GI:13538179  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Wojnowski, L. and Huster, E.  
TITLE Polymorphisms in the human hpxr gene and their use in diagnostic and therapeutic applications  
JOURNAL Patent: WO 0120026-A 32 22-MAR-2001; Epidauros Biotechnologie AG (DE)

FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="artificial sequence"

ORIGIN  
Query Match 44.0%; Score 8.8; DB 2; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.2e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13  
Db 1 CCCAGGTGAGG 12

RESULT 34  
LOCUS AX136994 12 bp DNA linear PAT 30-MAY-2001  
DEFINITION Sequence 68 from Patent EP1088500.  
ACCESSION AX136994  
VERSION AX136994.1 GI:14273341  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Huster, E., Wojnowski, L. and Eiselt, R.  
TITLE Polymorphisms in the human cyp3a4, cyp3a7 and hpxr genes and their use in diagnostic and therapeutic applications  
JOURNAL Patent: EP 1088500-A 68 04-APR-2001; Epidauros Biotechnologie AG (DE)

FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DNA"

ORIGIN
Query Match      44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.2e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGCAAG 13
Db 1 CCCAGGTGAGG 12

RESULT 35
BD257601/c
LOCUS      17 bp      DNA      linear      PAT 04-NOV-2005
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD257601
VERSION    BD257601.1 GI:33067371
KEYWORDS  JP 2002541795-A/5394.
SOURCE    unidentified
ORGANISM  unidentified
REFERENCE  1 (bases 1 to 17)
AUTHORS   Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE     Regulation of repressor genes using nucleic acid molecules
JOURNAL   Patent: JP 2002541795-A 5394 10-DEC-2002;
          RIBOZYME PHARMACEUTICALS INC
COMMENT   OS Eukaryote
          PN JP 2002541795-A/5394
          PD 10-DEC-2002
          PF 11-APR-2000 JP 2000611654
          PR 12-APR-1999 US 60/129390
          PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
          C12N15/09, A61K38/00, A61P43/00, A61P43/00, C12N5/10, PC
          C12P21/02,
          PC
          C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
          C12R1:91),
          PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
          PC A61K37/02,
          PC (C12N5/00, C12R1:91)
          CC Regulation of repressor genes using nucleic acid molecules FH
          Key Location/Qualifiers
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          /organism='Eukaryote'.
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          /mol_type='unassigned DNA'
          /db_xref='taxon:32644'

ORIGIN
Query Match      62.0%; Score 12.4; DB 2; Length 17;
Score over Length 72.9%;
Best Local Similarity 92.9%; Pred. No. 9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17
Db 15 CCAGTTGAAGCTGC 2

RESULT 37
BD066223
LOCUS      14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066223
VERSION    BD066223.1 GI:22611826
KEYWORDS  JP 2001511000-A/858.
SOURCE    unidentified
ORGANISM  unidentified
REFERENCE  1 (bases 1 to 14)
AUTHORS   Schlingensiepen, K.H. and Brysch, W.
TITLE     An antisense oligonucleotide preparation method
JOURNAL   Patent: JP 2001511000-A 858 07-AUG-2001;
          BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT   OS Unknown
          PN JP 2001511000-A/858
          PD 07-AUG-2001
          PF 30-JAN-1998 JP 1998532533
          PR 31-JAN-1997 EP 97101531.8
          PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
          PC C12N15/11, C07H21/04, A61K31/70
          CC An antisense oligonucleotide preparation method FH
          Key Location/Qualifiers
          FT source 1..14
          /organism='Unknown'.
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          /organism='unidentified'
          /mol_type='genomic DNA'
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ORIGIN	Matches	10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Query Match	QY	7	GTGAAGTTG	16						
Score over Length										
Best Local Similarity	Db	5	GTGAAGTTG	14						
Matches		10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
RESULT 38										
LOCUS	AR774929				14 bp	DNA	linear			PAT 08-DEC-2005
DEFINITION	Sequence 858 from patent US 6972171.									
ACCESSION	AR774929									
VERSION	AR774929.1				GI:83352193					
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 14)									
AUTHORS	Schlingensiepen,K.-H. and Brysch,W.									
TITLE	Antisense oligonucleotide preparation method									
JOURNAL	Patent: US 6972171-A 858 06-DEC-2005;									
COMMENT	Biognostik Ges. fur biomolekulare Diagnostik mbH; Gottingen;									
FEATURES	EPX;									
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ORIGIN										
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Score over Length					71.4%;					
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Matches		10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	7	GTGAAGTTG	16							
Db	5	GTGAAGTTG	14							
RESULT 39										
LOCUS	A88710				14 bp	DNA	linear			PAT 22-JAN-2000
DEFINITION	Sequence 858 from Patent WO9833904.									
ACCESSION	A88710									
VERSION	A88710.1				GI:6737280					
KEYWORDS	unidentified									
SOURCE	unclassified sequences.									
ORGANISM	unclassified sequences.									
REFERENCE	1 (bases 1 to 14)									
AUTHORS	Brysch,W. and Schlingensiepen,K.									
TITLE	AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD									
JOURNAL	Patent: WO 9833904-A 858 06-AUG-1998;									
COMMENT	BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)									
FEATURES	Location/Qualifiers									
source	1..14									
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/mol_type="unassigned DNA"										
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ORIGIN										
Query Match					50.0%;	Score 10;	DB 2;	Length 14;		
Score over Length					71.4%;					
Best Local Similarity					100.0%;	Pred. No. 2e+06;				
Matches		10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	7	GTGAAGTTG	16							
Db	5	GTGAAGTTG	14							
RESULT 40										
LOCUS	AR774929				14 bp	DNA	linear			PAT 08-DEC-2005
DEFINITION	Sequence 858 from patent US 6972171.									
ACCESSION	AR774929									
VERSION	AR774929.1				GI:83352193					
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 14)									
AUTHORS	Schlingensiepen,K.-H. and Brysch,W.									
TITLE	Antisense oligonucleotide preparation method									
JOURNAL	Patent: US 6972171-A 858 06-DEC-2005;									
COMMENT	Biognostik Ges. fur biomolekulare Diagnostik mbH; Gottingen;									
FEATURES	EPX;									
source	Location/Qualifiers									
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/mol_type="genomic DNA"										
ORIGIN										
Query Match					50.0%;	Score 10;	DB 2;	Length 14;		
Score over Length					71.4%;					
Best Local Similarity					100.0%;	Pred. No. 2e+06;				
Matches		10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	7	GTGAAGTTG	16							
Db	5	GTGAAGTTG	14							
RESULT 41										
LOCUS	CS508144/c				17 bp	RNA	linear			PAT 02-APR-2007
DEFINITION	Sequence 3654 from Patent EP1767632.									
ACCESSION	CS508144									
VERSION	CS508144.1				GI:138751678					
KEYWORDS	Homo sapiens (human)									
SOURCE	Homo sapiens									
ORGANISM	Homo sapiens									
REFERENCE	1									
AUTHORS	Escobedo,J., Pavco,P., Sandburg,J., McSwiggen,J., Stinchcomb,D. and Gordon,G.									
TITLE	A method for local administration of synthetic double-stranded oligonucleotides targeting a VEGF receptor									
JOURNAL	Patent: EP 1767632-A 3654 28-MAR-2007;									
COMMENT	Sirna Therapeutics, Inc. (US); Novartis Vaccines and Diagnostics, Inc. (US)									
FEATURES	Location/Qualifiers									
source	1..17									
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/db_xref="taxon:9606"										
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Query Match					60.0%;	Score 12;	DB 2;	Length 17;		
Score over Length					70.6%;					
Best Local Similarity					100.0%;	Pred. No. 1.5e+05;				
Matches		12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	3	CCAGTTGAAGT	14							





LOCUS AR324245 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1647 from patent US 6566127.  
ACCESSION AR324245  
VERSION AR324245.1 GI:33710053  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1647 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 CCCAGTTGAAGT 14  
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Db 16 CCCAGTTGAAGT 5  
RESULT 47  
AR328851/c  
LOCUS AR328851 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 6253 from patent US 6566127.  
ACCESSION AR328851  
VERSION AR328851.1 GI:33714659  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 6253 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 CCCAGTTGAAGT 14  
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Db 15 CCCAGTTGAAGT 4  
RESULT 48  
AR328852/c  
LOCUS AR328852 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 6254 from patent US 6566127.  
ACCESSION AR328852  
VERSION AR328852.1 GI:33714660  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
LOCUS AR324245 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1647 from patent US 6566127.  
ACCESSION AR324245  
VERSION AR324245.1 GI:33710053  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1647 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
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Score over Length 70.6%;  
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Qy 3 CCCAGTTGAAGT 14  
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Db 17 CCCAGTTGAAGT 6  
RESULT 50  
AR597705/c  
LOCUS AR597705 17 bp RNA linear PAT 15-DEC-2004  
DEFINITION Sequence 1647 from patent US 6818447.  
ACCESSION AR597705  
VERSION AR597705.1 GI:56648719  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6818447-A 1647 16-NOV-2004;  
Sirna Therapeutics, Inc.; Boulder, CO  
FEATURES  
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Query Match 60.0%; Score 12; DB 2; Length 17;  
Score over Length 70.6%;  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 CCCAGTTGAAGT 14  
|||||  
Db 17 CCCAGTTGAAGT 6  
RESULT 49  
AR597704/c  
LOCUS AR597704 17 bp RNA linear PAT 15-DEC-2004  
DEFINITION Sequence 1646 from patent US 6818447.  
ACCESSION AR597704  
VERSION AR597704.1 GI:56648718  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6818447-A 1646 16-NOV-2004;  
Sirna Therapeutics, Inc.; Boulder, CO  
FEATURES  
source  
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ORIGIN  
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Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
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Qy 3 CCCAGTTGAAGT 14  
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Db 12 CCCAGTTGAAGT 1

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ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 16 CCCAGTTGAAGT 5

RESULT 51
LOCUS AR841343 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 1646 from patent US 7034009.
ACCESSION AR841343
VERSION AR841343.1 GI:111928896
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 1646 25-APR-2006;
Sirta Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
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source Location/Qualifiers
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Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 17 CCCAGTTGAAGT 6

RESULT 52
LOCUS AR841344/c 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 1647 from patent US 7034009.
ACCESSION AR841344
VERSION AR841344.1 GI:111928897
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 1647 25-APR-2006;
Sirta Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
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source Location/Qualifiers
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Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 12 CCCAGTTGAAGT 5

RESULT 53
LOCUS AR845950 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 6253 from patent US 7034009.
ACCESSION AR845950
VERSION AR845950.1 GI:111933503
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 6253 25-APR-2006;
Sirta Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
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Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 54
LOCUS AR845951 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 6254 from patent US 7034009.
ACCESSION AR845951
VERSION AR845951.1 GI:111933504
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 6254 25-APR-2006;
Sirta Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned RNA"
ORIGIN
Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 12 CCCAGTTGAAGT 1
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RESULT 55
LOCUS AR848268 17 bp RNA linear PAT 10-AUG-2006
DEFINITION Sequence 8571 from patent US 7034009.
ACCESSION AR848268
VERSION AR848268.1 GI:111935821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Eacobedo,J.
TITLE Enzymatic nucleic acid-mediated treatment of ocular diseases or
conditions related to levels of vascular endothelial growth factor
receptor (VEGF-R)
JOURNAL Patent: US 7034009-A 8571 25-APR-2006;
US;
Sirta Therapeutics, Inc. and Chiron Corporation; Boulder, CO;
US;
FEATURES
source Location/Qualifiers
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Query Match 60.0%; Score 12; DB 2; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCCAGTTGAAGT 14
Db 14 CCCAGTTGAAGT 3
RESULT 56
LOCUS AR101078 12 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 48 from patent US 6083694.
ACCESSION AR101078
VERSION AR101078.1 GI:12811876
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Hardy,J. and Goate,A.M.
TITLE Method for elucidation and detection of polymorphisms, splice
variants, and proximal coding mutations using intronic sequences of
the alzheimer's S182 gene
JOURNAL Patent: US 6083694-A 48 04-JUL-2000;
US;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAGTTG 16
Db 10 GTTGATGTTG 1
RESULT 57
LOCUS CS097732 12 bp DNA linear PAT 03-JUN-2005
DEFINITION Sequence 5 from Patent EP1500329.
ACCESSION CS097732
ORIGIN
Query Match 42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCCCAGTTG 10
Db 12 GCCCCAGTAG 3
RESULT 58
LOCUS CS097756 12 bp DNA linear PAT 03-JUN-2005
DEFINITION Sequence 29 from Patent EP1500329.
ACCESSION CS097756
VERSION CS097756.1 GI:66954158
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Green,L., Jakobovits,A., Klapholz,S., Kucherlapati,R. and Mendez,M.
TITLE Transgenic mammals having human Ig loci including plural VH and
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
JOURNAL Patent: EP 1500329-A 29 26-JAN-2005;
US;
Abgenix, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
ORIGIN
Query Match 42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCCCAGTTG 10
Db 12 GCCCCAGTAG 3
RESULT 59
LOCUS CS540753 12 bp DNA linear PAT 20-APR-2007
DEFINITION Sequence 132 from Patent WO2007012576.
ACCESSION CS540753
VERSION CS540753.1 GI:145581914
KEYWORDS
SOURCE unidentified
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ORGANISM      unidentified
unclassified sequences.
REFERENCE      1
AUTHORS        Zank, T. and Oswald, O.
TITLE          Combination of lipid metabolism proteins and uses thereof
JOURNAL        Patent: WO 2007012576-A 132 01-FEB-2007;
                BASF Plant Science GmbH (DE)
FEATURES       Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
                /note="Unidentified"

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 75.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 AGTTGAGTTGTC 17
Db      12 AGTGCAGTGGC 1
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        ||:|||||

RESULT 60
LOCUS      I07921
DEFINITION Sequence 33 from Patent EP 0159123.
ACCESSION  I07921
VERSION     I07921.1 GI:589374
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Hsiung,H.M., Schoner,R.G. and Schoner,B.E.
TITLE        Vectors for expressing bovine growth hormone derivatives
JOURNAL      Patent: EP 0159123-A2 33 23-OCT-1985;
                Location/Qualifiers
                1..12
                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GAAGTTGCCG 19
Db      12 GAAGTTGTCG 3
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        ||| |||||

RESULT 61
LOCUS      I34823
DEFINITION Sequence 16 from patent US 5599673.
ACCESSION  I34823
VERSION     I34823.1 GI:2087791
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Keating,M.T., Curran,M.E. and Wang,Q.
TITLE        Long QT syndrome genes
JOURNAL      Patent: US 5599673-A 16 04-FEB-1997;
                Location/Qualifiers
                1..12
                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GAAGTTGCCG 19
Db      12 GAAGTTGTCG 3
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        ||| |||||

RESULT 62
LOCUS      AR893297/c
DEFINITION Sequence 50 from patent US 7064244.
ACCESSION  AR893297
VERSION     AR893297.1 GI:112050376
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Jakobovits,A., Kucherlapati,R., Klapholz,S., Mendez,M.J. and
                Green,L.
TITLE        Transgenic mammals having human Ig loci including plural VH and VK
                regions and antibodies produced therefrom
JOURNAL      Patent: US 7064244-A 50 20-JUN-2006;
                Abgenix, Inc.; Fremont, CA;
                US;
                Location/Qualifiers
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ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTG 10
Db      12 GCCCCAGTAG 3
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        |||||

RESULT 63
LOCUS      AR893306/c
DEFINITION Sequence 59 from patent US 7064244.
ACCESSION  AR893306
VERSION     AR893306.1 GI:112050389
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Jakobovits,A., Kucherlapati,R., Klapholz,S., Mendez,M.J. and
                Green,L.
TITLE        Transgenic mammals having human Ig loci including plural VH and VK
                regions and antibodies produced therefrom
JOURNAL      Patent: US 7064244-A 59 20-JUN-2006;
                Abgenix, Inc.; Fremont, CA;
                US;
                Location/Qualifiers
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ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTG 10
Db      12 GCCCCAGTAG 3
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        |||||

RESULT 64
LOCUS      AR893306/c
DEFINITION Sequence 59 from patent US 7064244.
ACCESSION  AR893306
VERSION     AR893306.1 GI:112050389
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Jakobovits,A., Kucherlapati,R., Klapholz,S., Mendez,M.J. and
                Green,L.
TITLE        Transgenic mammals having human Ig loci including plural VH and VK
                regions and antibodies produced therefrom
JOURNAL      Patent: US 7064244-A 59 20-JUN-2006;
                Abgenix, Inc.; Fremont, CA;
                US;
                Location/Qualifiers
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ORIGIN
Query Match      42.0%; Score 8.4; DB 2; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 1.5e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTG 10
Db      12 GCCCCAGTAG 3
        |||||
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTG 10

Db 12 GCCCCAGTAG 3

Search completed: December 3, 2007, 17:42:36  
Job time : 2640 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:03:06 ; Search time 8518 Seconds  
(without alignments)  
182.695 Million cell updates/sec

Title: US-10-728-509-64  
Perfect score: 20  
Sequence: 1 gccccagttgaagttgcgt 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 66588504 seqs, 38904969350 residues

Word size : 1

Total number of hits satisfying chosen parameters: 570288

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_est13:\*  
12: gb\_est12:\*  
13: gb\_est11:\*  
14: gb\_est10:\*  
15: gb\_gss1:\*  
16: gb\_gss2:\*  
17: gb\_gss3:\*  
18: gb\_gss4:\*  
19: gb\_gss5:\*  
20: gb\_gss6:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	70.0	34	12 EH339462	EH339462 192096.29
2	13	65.0	46	1 AI026096	AI026096 ov94h09's
3	12	60.0	35	15 BH861691	BH861691 SALK_0878
4	12	60.0	35	18 ED597720	ED597720 SALK_0878
5	12	60.0	41	18 EI637387	EI637387 wang-VSVG
6	12	60.0	47	16 B2767445	B2767445 SALK_1388
7	11	55.0	28	17 DX593658	DX593658 Lewinski-
8	11	55.0	30	15 BH847383	BH847383 SALK_0531
9	11	55.0	32	17 CZ466560	CZ466560 C00562-3p
10	11	55.0	37	17 DX935836	DX935836 NEI segme
11	11	55.0	47	7 AV578677	AV578677 AV578677
12	11	55.0	47	12 EG532751	EG532751 RrLX4a42d
13	11	55.0	50	1 AU107927	AU107927 AU107927

14	11	55.0	50	14 DR979367	DR979367 SM014218
15	10	50.0	15	12 EH308710	EH308710 016929.32
16	10	50.0	19	18 EI596228	EI596228 Wang-VSVG
17	10	50.0	20	18 EI602830	EI602830 Wang-VSVG
18	10	50.0	21	11 EW471844	EW471844 trms3601b
19	10	50.0	22	11 EW623052	EW623052 rpbcr0111
20	10	50.0	24	18 EI599377	EI599377 Wang-VSVG
21	10	50.0	26	11 EW549125	EW549125 rain08.01
22	10	50.0	26	15 AZ361612	AZ361612 IM0106E18
23	10	50.0	28	12 EH306286	EH306286 000504.34
24	10	50.0	28	15 BH011467	BH011467 BG02165-5
25	10	50.0	28	18 EI618163	EI618163 Wang-VSVG
26	10	50.0	30	17 CZ476737	CZ476737 d09425-5p
27	10	50.0	30	18 EI525731	EI525731 Wang-VSVG
28	10	50.0	31	1 AA933748	AA933748 ot65e02.8
29	10	50.0	31	19 BX947252	BX947252 Arabidops
30	10	50.0	32	11 EW319155	EW319155 tlin24.h1
31	10	50.0	32	18 EI658957	EI658957 Wang-VSVG
32	10	50.0	34	18 EI609128	EI609128 Wang-VSVG
33	10	50.0	35	12 EH339546	EH339546 192331.28
34	10	50.0	36	15 AZ350375	AZ350375 IM0087G22
35	10	50.0	37	11 EW031990	EW031990 rctc20.f1
36	10	50.0	38	11 EW607208	EW607208 rsto233.g
37	10	50.0	38	18 EI558107	EI558107 Wang-VSVG
38	10	50.0	39	12 EC606644	EC606644 latexX04H
39	10	50.0	39	12 EH331535	EH331535 149871.07
40	10	50.0	39	14 DT011957	DT011957 VVH024H01
41	10	50.0	39	18 EI538658	EI538658 Wang-VSVG
42	10	50.0	40	1 AI097270	AI097270 qb88e05.x
43	10	50.0	40	18 EI538250	EI538250 Wang-VSVG
44	10	50.0	40	18 EI639555	EI639555 Wang-VSVG
45	10	50.0	41	1 AU013289	AU013289 AU013289

ALIGNMENTS

RESULT 1  
EH339462/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

EH339462 34 bp mRNA linear EST 01-MAR-2007  
192096.2950\_2002 3' ESTs from HeLa cell Homo sapiens cDNA 3', mRNA  
sequence.  
EH339462  
EH339462.1 GI:126408936  
EST.  
Homo sapiens (human)  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
Catarrhini; Homnidae; Homo.  
1 (bases 1 to 34)

Wu, O., Kim, Y.-C. and Wang, S.M.  
3' ESTs from HeLa cell  
Unpublished (2006)  
Contact: San Ming Wang  
Center for Functional Genomics  
ENH Research Institute, Northwestern University  
1001 University Place, Evanston, IL 60201, USA  
Tel: 224 364 7491  
Fax: 224 364 5003  
Email: swangl@northwestern.edu.

FEATURES  
Source

Location/Qualifiers  
1..34  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/sex="Female"  
/cell\_line="HeLa"  
/clone\_lib="3' ESTs from HeLa cell"  
/note="3' EST from cytoplasmic mRNA of HeLa cell collected  
by 454 pyrosequencing system"

ORIGIN

```

Query Match      70.0%; Score 14; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. NO. 2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17
DB 26 CCAGTTGAAGTTGC 13

RESULT 2
A1026096
LOCUS      A1026096
DEFINITION ov94h09.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1645025
3' similar to TR:Q62006 Q62006 OPA REPEAT ; contains element L1
repetitive element ;, mRNA sequence.
ACCESSION  A1026096
VERSION     A1026096
KEYWORDS    EST.
SOURCE      A1026096.1 GI:3241709
ORGANISM    Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1791 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1645025"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares_testis_NHT"
/note="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was prepared from mRNA obtained from
Clontech Laboratories, Inc., and primed with a Not I -
oligo(dT) primer [5',
TGTTCACATCGAGTGGAGCGCGCCCAATTTTITTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match      65.0%; Score 13; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. NO. 8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTCCCG 19
DB 34 GTTGAAGTCCCG 46

RESULT 3

```

```

BH861691
LOCUS      BH861691
DEFINITION SALK_087845 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_087845, genomic survey sequence.
ACCESSION  BH861691
VERSION     BH861691.1 GI:22097017
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 35)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome.
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
AT1g63280.
Class: TDNA tagged.
Location/Qualifiers
1. 35
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_087845"
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

Query Match      60.0%; Score 12; DB 15; Length 35;
Best Local Similarity 100.0%; Pred. NO. 3.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
DB 11 AGTTGAAGTTGC 22

RESULT 4
ED597720
LOCUS      ED597720
DEFINITION SALK_087845.54.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_087845.54.25.x, genomic
survey sequence.
ACCESSION  ED597720
VERSION     ED597720.1 GI:116596774
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 35)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

```



TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
The Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

source

1. .35  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone\_lib="SALK 087845.54.25.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN

Query Match 60.0%; Score 12; DB 18; Length 35;  
Best Local Similarity 100.0%; Pred. No. 3.1e+04; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;

Qy 6 AGTTGAAGTTGC 17

Db 11 AGTTGAAGTTGC 22

RESULT 5

EI637387/c

LOCUS

DEFINITION Wang-VSVGgfp-Jurkat-454-Mse-090835.2696.0476 linear GSS 25-APR-2007  
Wang-VSVGgfp-Jurkat-454-Mse Homo sapiens genomic, genomic survey sequence.

ACCESSION EI637387

VERSION EI637387.1

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Wang, G.P., Cluffi, A., Leipig, J., Berry, C.C. and Bushman, F.D.

TITLE HIV integration site selection: analysis by massively parallel pyrosequencing reveals association with epigenetic modifications

JOURNAL Genome Res. 17 (2007) In press

COMMENT Contact: Bushman, FD

Department of Microbiology  
University of Pennsylvania School of Medicine  
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA 19104-6076, USA

Tel: 215 573 8732

Fax: 215 573 4856

Email: [bushman@mail.med.upenn.edu](mailto:bushman@mail.med.upenn.edu)

Class: PCR fragment.

Location/Qualifiers

source

1. .41  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/cell\_type="Jurkat"  
/clone\_lib="Wang-VSVGgfp-Jurkat-454-Mse"

/note="Site 1: MseI; Amplified PCR products were directly sequenced using pyrosequencing as implemented by 454 Life Sciences. An HIV-based vector transducing GFP and pseudotyped with VSV-G envelope was used."

ORIGIN

Query Match 60.0%; Score 12; DB 18; Length 41;  
Best Local Similarity 100.0%; Pred. No. 3.1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17

Db 12 AGTTGAAGTTGC 1

RESULT 6

BZ767445

LOCUS

DEFINITION BZ767445 47 bp DNA linear GSS 13-MAR-2003  
SALK 138868.42.60.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_138868.42.60.x, genomic survey sequence.

ACCESSION BZ767445

VERSION BZ767445.1

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 47)

AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J. and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL Arabidopsis Genome

COMMENT Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: [ecker@salk.edu](mailto:ecker@salk.edu)

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At2g37810.

Class: TDNA tagged.

Location/Qualifiers

source

1. .47

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone\_lib="SALK 138868.42.60.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN

Query Match 60.0%; Score 12; DB 16; Length 47;  
Best Local Similarity 100.0%; Pred. No. 3.1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16

Db 4 CAGTTGAAGTTG 15

RESULT 7

DX593658



Sequence orientation is forward strand relative to 5' end of piggyBac element.  
 The piggyBac insertion position is unspecified in the 32 bases.  
 This insertion position refers to the first base of the 4 base TTAA target recognition sequence.  
 Class: transposon insertion site.

#### FEATURES

Location/Qualifiers  
 1..32  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /strain="isogenic w- strain"  
 /db\_xref="taxon:7227"  
 /clone\_lib="Exelixis piggyBac PB insertions"  
 /note="Vector: piggyBac PB (GenBank accession number AY151146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

#### ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16

Db 28 AGTTGAAGTTG 18

RESULT 10  
 DX935836  
 LOCUS  
 DEFINITION  
 NEI segment 622 Neanderthal genomic library NEI Homo sapiens neanderthalensis genomic, genomic survey sequence.

ACCESSION  
 DX935836

VERSION  
 DX935836.1 GI:113930415

KEYWORDS  
 GSS.

SOURCE  
 Homo sapiens neanderthalensis

ORGANISM  
 Homo sapiens neanderthalensis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

Catarrhini; Homnidae; Homo.

1 (bases 1 to 37)

Noonan,J.P., Coop,G., Kudaravalli,S., Smith,D., Krause,J.,

Alessi,J., Chen,F., Platt,D., Paabo,S., Pritchard,J.K. and

Rubin,E.M.

Sequencing and Analysis of Neanderthal Genomic DNA

Science 314 (5802), 1113-1118 (2006)

17110569

Contact: Noonan JP

Genomics Division

Lawrence Berkeley National Lab/US DOE Joint Genome Institute

84R0171, 1 Cyclotron Road, Berkeley, CA 94720

Email: jnoonan@lbl.gov

Generated by pyrosequencing

Class: shotgun.

Location/Qualifiers

1..37

/organism="Homo sapiens neanderthalensis"

/mol\_type="genomic DNA"

/sub\_species="neanderthalensis"

/db\_xref="taxon:63221"

#### FEATURES

source

#### ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCC 18

Db 4 TTGAAGTTGCC 14

#### RESULT 11

AV578677/c

LOCUS

DEFINITION

AV578677 Abe mouse ES cell Mus musculus cDNA clone 1990525EK02G01,

mRNA sequence.

ACCESSION

AV578677

VERSION

AV578677.1 GI:141299656

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

1 (bases 1 to 47)

Fukumura,R., Araki,R., Takahashi,H., Tsutsumi,Y., Ohhata,T. and

Abe,M.

Murine ES cells EST Project

Unpublished (2007)

Contact: Masumi Abe

Dept. of Biology and Oncology

National Institute of Radiological Sciences

Anagawa 4-9-1, Inage-ku, Chiba, 263-8555, Japan

Tel: 81-43-206-3219

Fax: 81-43-251-4593

Email: abemasu@nirs.go.jp.

Location/Qualifiers

1..47

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="1990525EK02G01"

/cell\_type="ES"

/cell\_line="E14"

/clone\_lib="Abe mouse ES cell"

/note="Vector: pSPORT 1 (GibcoBRL); Site 1: Sal I; Site 2:

Not I; 1st strand cDNA was primed with a Not I - oligo (dT)

primer [5'-CAGCGCGCGCTTTTTTTTTTTT-3'];

double-stranded cDNA was ligated to Sal I adaptors

[5'-TCGACCCACGCTCG-3'], digested with Not I and cloned

into the Sal I and Not I sites of pSPORT 1 vector.

Average insert size: 0.7 kb (range 0.2-1.3 kb); Sequence

primer: T7 [5'-TAATACGACTCACTATAGG-3']; Primary library,

non-amplified."

#### ORIGIN

Query Match 55.0%; Score 11; DB 7; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16

Db 36 AGTTGAAGTTG 26

#### RESULT 12

EG532751/c

LOCUS

DEFINITION

EG532751 RrLX4a4223f1 250DPH (.) Rutillus rutilus cDNA clone 42d22 5' LD,

mRNA sequence.

ACCESSION

EG532751

<p> <b>VERSION</b>  <b>KEYWORDS</b>  <b>SOURCE</b>  <b>ORGANISM</b> </p> <p> <b>REFERENCE</b>  <b>AUTHORS</b>  <b>TITLE</b>  <b>JOURNAL</b>  <b>COMMENT</b> </p>	<p> <b>FEATURES</b>  <b>source</b> </p> <p> <b>ORIGIN</b> </p> <p> <b>RESULT 13</b>  <b>AUI07927</b>  <b>LOCUS</b>  <b>DEFINITION</b>  <b>ACCESSION</b>  <b>VERSION</b>  <b>KEYWORDS</b>  <b>SOURCE</b>  <b>ORGANISM</b> </p> <p> <b>REFERENCE</b>  <b>AUTHORS</b>  <b>TITLE</b>  <b>JOURNAL</b>  <b>PUBLISHED</b>  <b>COMMENT</b> </p>	<p> <b>FEATURES</b>  <b>source</b> </p> <p> <b>ORIGIN</b> </p> <p> <b>RESULT 14</b>  <b>DR979367</b>  <b>LOCUS</b>  <b>DEFINITION</b>  <b>ACCESSION</b>  <b>VERSION</b>  <b>KEYWORDS</b>  <b>SOURCE</b>  <b>ORGANISM</b> </p> <p> <b>REFERENCE</b>  <b>AUTHORS</b>  <b>TITLE</b>  <b>JOURNAL</b>  <b>PUBLISHED</b>  <b>COMMENT</b> </p>	<p> <b>FEATURES</b>  <b>source</b> </p> <p> <b>ORIGIN</b> </p> <p> <b>RESULT 13</b>  <b>AUI07927</b>  <b>LOCUS</b>  <b>DEFINITION</b>  <b>ACCESSION</b>  <b>VERSION</b>  <b>KEYWORDS</b>  <b>SOURCE</b>  <b>ORGANISM</b> </p> <p> <b>REFERENCE</b>  <b>AUTHORS</b>  <b>TITLE</b>  <b>JOURNAL</b>  <b>PUBLISHED</b>  <b>COMMENT</b> </p>	<p> <b>FEATURES</b>  <b>source</b> </p> <p> <b>ORIGIN</b> </p> <p> <b>RESULT 14</b>  <b>DR979367</b>  <b>LOCUS</b>  <b>DEFINITION</b>  <b>ACCESSION</b>  <b>VERSION</b>  <b>KEYWORDS</b>  <b>SOURCE</b>  <b>ORGANISM</b> </p> <p> <b>REFERENCE</b>  <b>AUTHORS</b>  <b>TITLE</b>  <b>JOURNAL</b>  <b>PUBLISHED</b>  <b>COMMENT</b> </p>
<p>             RG532751.1 GI:116520154              EST.              Rutulus rutulus (roach minnow)              Rutulus rutulus              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;              Actinopterygii; Neopterygii; Teleostei; Ostariophysi;              Cypriniformes; Cyprinidae; Rutulus.              1 (bases 1 to 47)              Chatziandreou,N., Williams,D., Li,W., Lange,A., Chidgey,L.,              Tyler,C.R. and Cousins,A.R.              Endocrine disruption in roach              Unpublished (2007)              Contact: Andrew R. Cousins              Laboratory for Environmental Gene Regulation              University of Liverpool              School of Biological Sciences, The Biosciences Building, Crown              Street, Liverpool, United Kingdom, L69 7ZB              Tel: +44(0)151-795-4510              Fax: +44(0)151-795-4431              Email: cousins@liverpool.ac.uk              Vector has been trimmed from this EST.              Plate: 42 row: d column: 22              Seq primer: pTriplex2 5' LD 3' LD              High quality sequence stop: 47.              Location/Qualifiers              1..47              /organism="Rutulus rutulus"              /mol_type="mRNA"              /db_xref="taxon:48668"              /clone="42d22"              /sex="Male"              /clone_lib="250DPH (.)"              /notes="Organ: Gonads; Vector: pTriplex2; Site 1: Sfil              GGCCATTAGGCC; Site 2: Sfil GGCGCCCTCGGC; cDNA library              prepared from roach 250dph (days post hatch) exposed              (exposed to EDCs)"           </p>	<p>             Query Match 55.0%; Score 11; DB 12; Length 47;              Best Local Similarity 100.0%; Pred. No. 1.2e+05;              Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              QY 10 GAAGTTGCCCT 20                                 DB 32 GAAGTTGCCCT 22           </p>	<p>             Query Match 55.0%; Score 11; DB 12; Length 47;              Best Local Similarity 100.0%; Pred. No. 1.2e+05;              Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              QY 10 GAAGTTGCCCT 20                                 DB 32 GAAGTTGCCCT 22           </p>	<p>             Query Match 55.0%; Score 11; DB 12; Length 47;              Best Local Similarity 100.0%; Pred. No. 1.2e+05;              Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              QY 10 GAAGTTGCCCT 20                                 DB 32 GAAGTTGCCCT 22           </p>	<p>             Query Match 55.0%; Score 11; DB 12; Length 47;              Best Local Similarity 100.0%; Pred. No. 1.2e+05;              Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              QY 10 GAAGTTGCCCT 20                                 DB 32 GAAGTTGCCCT 22           </p>
<p>             AUI07927              Sugano Homo sapiens cDNA library              50 bp mRNA linear EST 17-APR-2006              ZR61994 5', mRNA sequence.              AUI07927              AUI07927.1 GI:13557449              EST.              Homo sapiens (human)              Homo sapiens              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;              Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;              Catarrhini; Hominoidea; Homo.              1 (bases 1 to 50)              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.              Diverse transcriptional initiation revealed by fine, large-scale              mapping of mRNA start sites              ENBO Rep. 2 (5), 388-393 (2001)              11375929              Contact: Yutaka Suzuki              Department of Virology              Institute of Medical Science, University of Tokyo              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan              Tel: 81-3-5449-5343           </p>	<p>             Query Match 55.0%; Score 11; DB 14; Length 50;              Best Local Similarity 100.0%; Pred. No. 1.2e+05;              Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              QY 7 GTTGAAGTTGC 17                                 DB 11 GTTGAAGTTGC 21           </p>	<p>             Query Match 55.0%; Score 11; DB 1; Length 50;              Best Local Similarity 100.0%; Pred. No. 1.2e+05;              Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              QY 7 GTTGAAGTTGC 17                                 DB 11 GTTGAAGTTGC 21           </p>	<p>             Query Match 55.0%; Score 11; DB 1; Length 50;              Best Local Similarity 100.0%; Pred. No. 1.2e+05;              Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              QY 7 GTTGAAGTTGC 17                                 DB 11 GTTGAAGTTGC 21           </p>	<p>             Query Match 55.0%; Score 11; DB 1; Length 50;              Best Local Similarity 100.0%; Pred. No. 1.2e+05;              Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              QY 7 GTTGAAGTTGC 17                                 DB 11 GTTGAAGTTGC 21           </p>

Matches 11; . Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAA 12  
|||||  
Db 21 CCCAGTTGAA 31

RESULT 15  
EH308710  
LOCUS EH308710 15 bp mRNA linear EST 01-MAR-2007  
DEFINITION 016929\_3219\_3561 3' ESTs from HeLa cell Homo sapiens cDNA 3', mRNA  
sequence.  
ACCESSION EH308710  
VERSION EH308710  
KEYWORDS EST. GI:126373552  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
1 (bases 1 to 15)  
Wu, Q., Kim, Y.C. and Wang, S.M.  
3' ESTs from HeLa cell  
Unpublished (2006)  
Contact: San Ming Wang  
Center for Functional Genomics  
ENH Research Institute, Northwestern University  
1001 University Place, Evanston, IL 60201, USA  
Tel: 224 364 7491  
Fax: 224 364 5003  
Email: swangl@northwestern.edu.

FEATURES  
source  
1..15  
Location/Qualifiers  
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/clone\_lib="3' ESTs from HeLa cell"  
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by 454 pyrosequencing system"

ORIGIN

Query Match 50.0%; Score 10; DB 12; Length 15;  
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCC 18  
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Db 3 TGAAGTTGCC 12

Search completed: December 3, 2007, 18:25:11  
Job time : 8525 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:01:39 ; Search time 1236 Seconds  
(without alignments)  
174.683 Million cell updates/sec

Title: US-10-728-509-64  
Perfect score: 20  
Sequence: 1 gccccagttgaagtgcgcgt 20

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 9073515 seqs, 5397694045 residues

Word size : 1  
Total number of hits satisfying chosen parameters: 9333772

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

- Database :
- 1: Geneseqn\_200711.\*
  - 2: Geneseqn1990s.\*
  - 3: Geneseqn2000.\*
  - 4: Geneseqn2001a.\*
  - 5: Geneseqn2001b.\*
  - 6: Geneseqn2002a.\*
  - 7: Geneseqn2002b.\*
  - 8: Geneseqn2003a.\*
  - 9: Geneseqn2003b.\*
  - 10: Geneseqn2003c.\*
  - 11: Geneseqn2003d.\*
  - 12: Geneseqn2004a.\*
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  - 14: Geneseqn2004c.\*
  - 15: Geneseqn2004d.\*
  - 16: Geneseqn2005a.\*
  - 17: Geneseqn2005b.\*
  - 18: Geneseqn2005c.\*
  - 19: Geneseqn2006a.\*
  - 20: Geneseqn2006b.\*
  - 21: Geneseqn2006c.\*
  - 22: Geneseqn2007.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	8	ADA20891 Human BAX
2	18	90.0	20	8	ADA20892 Human BAX
c 3	17	85.0	22	7	ABV73748 Human Bax
4	17	85.0	24	19	AEJ10477 Target nu
5	17	85.0	24	19	AEJ10484 Target nu
c 6	17	85.0	42	19	AEJ10483 Circulariz
c 7	17	85.0	44	19	AEJ10476 Circulariz
c 8	17	85.0	44	19	AEJ10482 Circulariz
c 9	17	85.0	45	19	AEJ10475 PGR probe
10	16	80.0	20	8	ABX13068 Human bax
11	16	80.0	20	8	ADA20946 Mouse BAX

12	16	80.0	20	17	AED12216	Aed12216 Bax (huma
13	16	80.0	20	19	AEJ97326	Aej97326 RT-PCR pr
14	16	80.0	20	19	AEK58344	Aek58344 Interfero
c 15	16	80.0	22	19	AEH24548	Aeh24548 BAX gene
c 16	16	80.0	22	19	AEH24560	Aeh24560 BAX forwa
c 17	16	80.0	22	19	AEJ10474	Aej10474 Antisense
18	15	75.0	18	8	ADA20832	Ada20832 Human BCL
19	15	75.0	25	20	AF227061	Af227061 Saccharom
20	15	75.0	25	21	AGC11439	Agc11439 Saccharom
c 21	14	70.0	25	17	AED15910	Aed15910 P. putida
22	14	70.0	37	2	AAV85651	Aav85651 LRP5 exon
c 23	13	65.0	20	6	AB231305	Ab231305 Candida a
24	13	65.0	20	8	ADA20945	Ada20945 Mouse BAX
25	13	65.0	20	8	ADA20947	Ada20947 Mouse BAX
c 26	13	65.0	25	13	ABO20836	Abo20836 Mouse gen
c 27	13	65.0	25	17	AEK84167	Aek84167 Human MMP
28	13	65.0	25	20	AF281835	Af281835 Saccharom
29	13	65.0	25	21	AGC66213	Agc66213 Saccharom
30	13	65.0	29	10	ADK17509	Adk17509 SB varian
c 31	13	65.0	50	6	AB205963	Ab205963 Human leu
c 32	13	65.0	50	6	AB206328	Ab206328 Human leu
c 33	13	65.0	50	19	AFG04299	Afg04299 SNP found
c 34	12	60.0	15	2	AAK75721	Aax75721 Human flt
c 35	12	60.0	17	2	AAK71130	Aax71130 Human KDR
c 36	12	60.0	17	2	AAK71129	Aax71129 Human KDR
c 37	12	60.0	17	8	ABE61076	Aeb61076 Human VEG
c 38	12	60.0	19	19	AEK84167	Aek84167 Human MMP
39	12	60.0	19	19	AEK84373	Aek84373 Human MMP
c 40	12	60.0	20	4	AAH26103	Aah26103 VEGF rece
c 41	12	60.0	21	13	ADQ93237	Adq93237 3-alpha-h
c 42	12	60.0	21	13	ADQ93231	Adq93231 3-alpha-h
c 43	12	60.0	21	13	ADQ93236	Adq93236 3-alpha-h
c 44	12	60.0	21	13	ADQ93232	Adq93232 3-alpha-h
c 45	12	60.0	21	13	ADQ93235	Adq93235 3-alpha-h

ALIGNMENTS

RESULT 1

ID	ADA20891	standard; DNA; 20 BP.
XX		
AC	ADA20891;	
XX		
DT	20-NOV-2003	(first entry)
XX		
DE	Human BAX chimeric phosphorothioate oligonucleotide	SEQ ID NO:64.
XX		
KW	BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;	
KW	anticonvulsant; ophthalmologic; antidiabetic; virucide;	
KW	antisense therapy; BAX antagonist; BAX inhibitor;	
KW	familial amyotrophic lateral sclerosis; Alzheimer's disease;	
KW	Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;	
KW	diabetes-associated ocular disorder; scrapie infection;	
KW	aberrant apoptosis; human; phosphorothioate; ss.	
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OS	Synthetic.	
OS	Homo sapiens.	
XX		
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FT	modified_base	16..20
FT		/tag= c
FT		/mod_base= OTHER

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FT      /note= "2'-O-methoxyethyls"
XX      WO2003008543-A2.
XX      30-JAN-2003.
XX      13-JUL-2002; 2002WO-US022417.
XX      17-JUL-2001; 2001US-00908147.
XX      (ISIS-) ISIS PHARM INC.
XX      Zhang H, Watt AT;
XX      WPI; 2003-239321/23.
XX      New antisense compounds, useful for modulating the expression of BCL2-
XX      associated X (BAX) protein or for treating a disease or condition
XX      associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
XX      or Alzheimer's disease.
XX      Claim 3; Page 86; 139pp; English.
XX      The present invention describes a compound (I) 8-50 nucleobases in length
XX      targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
XX      protein, where the compound specifically hybridises with the nucleic acid
XX      molecule encoding BAX protein and inhibits the expression of BAX protein.
XX      The compound specifically hybridises with at least 8-nucleobase portion
XX      of an active site on a nucleic acid molecule encoding BAX protein. Also
XX      described: (1) a composition comprising (I) and a pharmaceutical carrier
XX      or diluent; (2) inhibiting the expression of BAX protein in cells or
XX      tissues comprising contacting the cells or tissues with (I); and (3)
XX      treating an animal having a disease or condition associated with BAX
XX      protein comprising administering to the animal (I) so that expression of
XX      BAX protein is inhibited. (I) has neurotropic, neuroprotective,
XX      antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
XX      virucide activities, and can be used in antisense therapy, and as a BAX
XX      antagonist. The antisense compounds (I) are useful for modulating the
XX      expression of BAX protein, and for treating a disease or condition
XX      associated with BAX protein, e.g. familial amyotrophic lateral
XX      sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
XX      cartilage-hair hyperplasia, diabetes-associated ocular disorders or
XX      scrapie infection, or a condition that arises from aberrant apoptosis.
XX      The compounds are useful as research reagents and in diagnostics. The
XX      present sequence represents a human BAX chimeric phosphorothioate
XX      oligonucleotide, which is used in an example from the present invention.
XX      Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
XX      Query Match 100.0%; Score 20; DB 8; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 0.15;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      Qy 1 GCCCAGTGAAGTTCGGT 20
XX      Db 1 GCCCAGTGAAGTTCGGT 20
XX      RESULT 2
XX      ADA20892
XX      ID ADA20892 standard; DNA; 20 BP.
XX      AC ADA20892;
XX      DT 20-NOV-2003 (first entry)
XX      DE Human BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:65.
XX      EC BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;
XX      EW anticonvulsant; ophthalmological; antidiabetic; virucide;
XX      FW antisense therapy; BAX antagonist; BAX inhibitor;
XX      HW familial amyotrophic lateral sclerosis; Alzheimer's disease;
XX      HW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;

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KW      diabetes-associated ocular disorder; scrapie infection;
KW      aberrant apoptosis; human; phosphorothioate; ss.
XX      Synthetic.
XX      OS Homo sapiens.
XX      Key Location/Qualifiers
XX      modified_base 1..20
XX      /tag= b
XX      /mod_base= OTHER
XX      /note= "phosphorothioate linkages, and all cytidine
XX      residues are 5-methylcytidines"
XX      modified_base 1..5
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XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyls"
XX      modified_base 16..20
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XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyls"
XX      WO2003008543-A2.
XX      30-JAN-2003.
XX      13-JUL-2002; 2002WO-US022417.
XX      17-JUL-2001; 2001US-00908147.
XX      (ISIS-) ISIS PHARM INC.
XX      Zhang H, Watt AT;
XX      WPI; 2003-239321/23.
XX      New antisense compounds, useful for modulating the expression of BCL2-
XX      associated X (BAX) protein or for treating a disease or condition
XX      associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
XX      or Alzheimer's disease.
XX      Claim 3; Page 86; 139pp; English.
XX      The present invention describes a compound (I) 8-50 nucleobases in length
XX      targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
XX      protein, where the compound specifically hybridises with the nucleic acid
XX      molecule encoding BAX protein and inhibits the expression of BAX protein.
XX      The compound specifically hybridises with at least 8-nucleobase portion
XX      of an active site on a nucleic acid molecule encoding BAX protein. Also
XX      described: (1) a composition comprising (I) and a pharmaceutical carrier
XX      or diluent; (2) inhibiting the expression of BAX protein in cells or
XX      tissues comprising contacting the cells or tissues with (I); and (3)
XX      treating an animal having a disease or condition associated with BAX
XX      protein comprising administering to the animal (I) so that expression of
XX      BAX protein is inhibited. (I) has neurotropic, neuroprotective,
XX      antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
XX      virucide activities, and can be used in antisense therapy, and as a BAX
XX      antagonist. The antisense compounds (I) are useful for modulating the
XX      expression of BAX protein, and for treating a disease or condition
XX      associated with BAX protein, e.g. familial amyotrophic lateral
XX      sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
XX      cartilage-hair hyperplasia, diabetes-associated ocular disorders or
XX      scrapie infection, or a condition that arises from aberrant apoptosis.
XX      The compounds are useful as research reagents and in diagnostics. The
XX      present sequence represents a human BAX chimeric phosphorothioate
XX      oligonucleotide, which is used in an example from the present invention.
XX      Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
XX      Query Match 90.0%; Score 18; DB 8; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 2;
XX      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      Qy 1 GCCCAGTGAAGTTCGCC 18

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<p>Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0</p> <p>QY 4 CCAGTTGAAGTTCCTG 20       Db 22 CCAGTTGAAGTTCCTG 6</p> <p>RESULT 4 AEJ10477 ID AEJ10477 standard; DNA; 24 BP. XX AC AEJ10477; XX DT 07-SEP-2006 (first entry) XX DE Target nucleic acid for nuclease-based cleavage reaction PG-RCA. XX KW DNA detection; microorganism detection; SNP detection; KW epigenetic modification; diagnostic; RNA detection; DNA amplification; KW DNA methylation; gene amplification; primer extension; ss; KW DNA-RNA hybrid. XX OS Synthetic. XX FH Key Location/Qualifiers FT modified_base 22..24 FT /*tag= a FT /mod_base= 2'-O-methyluridine XX PN WO2006074162-A2. XX PD 13-JUL-2006. XX PF 04-JAN-2006; 2006WO-US000086. XX PR 04-JAN-2005; 2005US-0641255P. XX PR 14-JUL-2005; 2005US-0699340P. XX PA (HITB ) HITACHI CHEM CO LTD. PA (HITB ) HITACHI CHEM RES CENT INC. XX Murakami T; XX WPI; 2006-513365/52.</p>	<p>The present invention discloses a method of amplifying nucleic acid using primers and probes by rolling circle amplification method. The present invention comprises primer generation ? rolling circle amplification (PG-RCA) in which a ribbon probe is involved, allows the single step detection of nucleic acid sequences such as DNA and RNA sensitively and rapidly. This technology is easily applicable to detection of other biomolecules such as DNA methylation, single nucleotide polymorphism (SNP), protein and posttranslational modifications. PCR (primer generation reaction) is a reaction that is designed to produce at least one nucleic acid primer from a PCR initiation sequence of an RCR (rolling circle reaction) product and the resulting primer is designed to prime to a circular nucleic acid probe and initiate RCR. On the other hand, RCR is designed to produce concatenated sequence copies of the circular probe, in which the resulting product contains at least one PCR initiation sequence in every repeat sequence just like the initial reaction signal. The first and second nucleic acid primers are generated by one of nuclease-based cleavage reaction, strand displacement amplification, cleavage-initiated isothermal amplification, three-way junction isothermal amplification, three-way junction rolling circle reaction, binding assay using a nucleic acid labeled recognition agent and proximity assay. The method of nucleic acid detection using the present invention is useful for in vitro diagnostics and in pathogen detection.</p>
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<p>Match 3 GCCCCAGTTGAAGTTCCTG 20</p> <p>RESULT 3 ABV73748/c ID ABV73748 standard; DNA; 22 BP. XX AC ABV73748; XX DT 30-DEC-2002 (first entry) XX DE Human Bax sense PCR primer. XX KW Cell adhesion; apoptosis; peritoneum; Bax; human; vulnery; cytostatic; KW antiinflammatory; antiinfertility; gene therapy; PCR; primer; ss. XX OS Homo sapiens. XX PN WO200272130-A1. XX PD 19-SEP-2002. XX PF 11-MAR-2002; 2002WO-US007119. XX PR 13-MAR-2001; 2001US-0275349P. XX PA (UYWA-) UNIV WAYNE STATE. XX PI Diamond MP, Saed GM; XX DR WPI; 2002-740784/80. XX PT Preventing or remedying surgical adhesion, useful for preventing infection, pain or inflammation after surgery or during wound healing, by modulating apoptosis in peritoneal cells in a subject using Bax agonists or Bcl-2 antagonists.</p>	<p>Example 1; Page 16; 24pp; English.</p> <p>The present sequence is a sense primer for the human Bax gene coding region. Use with the antisense primer given in ABV73749 gives a 135 bp PCR product. Multiplex RT-PCR was used for the simultaneous amplification of Bcl-2, Bax and beta-actin mRNAs in peritoneal and adhesion fibroblasts in response to hypoxia. The results showed that adhesion fibroblasts have almost double the Bcl-2/Bax mRNA ratio as peritoneal fibroblasts. Hypoxia resulted in a 25% decrease in the Bcl-2/Bax ratio for normal peritoneum fibroblasts, indicating an increase in apoptosis. Hypoxia also resulted in a 33% increase in the Bcl-2/Bax ratio for adhesion fibroblasts, indicating a decrease in apoptosis. The Bcl-2/Bax ratio can determine whether cells die by apoptosis, or be protected from it. The higher the ratio, the lower the apoptosis rate. The invention provides a method for the prevention or remediation of surgical adhesion by modulating apoptosis in peritoneal, especially fibroblast, cells. The rate of apoptosis is increased using a therapeutic formulation comprising Bax, Bax enhancer (e.g. p53), Bax agonist, Bcl-2 inhibitor or Bcl-2 antagonist. A gene therapy method which introduces the p53 or Bax gene into the fibroblast cells may be used. Determination of the Bcl-2/Bax ratio can be used to determine whether a human subject, or an organ or tissue site, is predisposed to develop adhesions during or following surgery. The method is particularly useful for preventing the development of post-operative adhesions in of patients following surgery, e.g. ovarian cystectomy, laparoscopic or open cholecystectomy, colectomy, splenectomy, kidney transplantation, or caesarean section. It is also useful in preventing or eliminating cell proliferation or migration, infection or inflammation during the wound healing process, in preventing bowel obstruction, pain and infertility, in preventing pannus formation, or for treating inflammation</p>
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<p>Query Match 85.0%; Score 17; DB 7; Length 22; Best Local Similarity 100.0%; Pred. No. 7.5;</p>	<p>Sequence 22 BP; 5 A; 6 C; 5 G; 6 T; 0 U; 0 Other;</p>
---	--



CC The nucleotide sequence presented here is the target nucleic acid for  
 CC nuclease-based cleavage reaction PG-RCA.

XX Sequence 24 BP; 5 A; 5 C; 6 G; 5 T; 3 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGCCGT 20

Db 1 CCAGTTGAAGTTGCCGT 17

#### RESULT 5

AEJ10484

ID AEJ10484 standard; DNA; 24 BP.

XX AC AEJ10484;

DT 07-SEP-2006 (first entry)

XX Target nucleic acid used in PG-RCA using ribbon probe.

XX DNA detection; microorganism detection; SNP detection;  
 KW epigenetic modification; diagnostic; RNA detection; DNA amplification;  
 KW DNA methylation; gene amplification; primer extension; ss;  
 KW DNA-RNA hybrid.

XX Synthetic.

XX Key Location/Qualifiers

FT misc\_RNA 22..24

FT modified\_base /\*tag= a

FT /\*tag= b

FT /\*mod\_base= 2'-O-methyluridine

XX WO2006074162-A2.

PN 13-JUL-2006.

PD 04-JAN-2006; 2006WO-US000086.

PP 04-JAN-2005; 2005US-0641255P.

PR 14-JUL-2005; 2005US-0699340P.

XX (HITB ) HITACHI CHEM CO LTD.

PA (HITB ) HITACHI CHEM RES CENT INC.

XX Murakami T;

PI WPI; 2006-513365/52.

DR Amplifying nucleic acid, by combining a nucleic acid primer with a

XX polymerase and a circular nucleic acid probe, and producing a repeat of a

XX sequence copy of the circular nucleic acid probe.

XX Example 6; SEQ ID NO 16; 34pp; English.

XX The present invention discloses a method of amplifying nucleic acid using

XX primers and probes by rolling circle amplification method. The present

XX invention comprises primer generation ? rolling circle amplification (PG-

XX RCA) in which a ribbon probe is involved, allows the single step

XX detection of nucleic acid sequences such as DNA and RNA sensitively and

XX rapidly. This technology is easily applicable to detection of other

XX biomolecules such as DNA methylation, single nucleotide polymorphism

XX (SNP), protein and posttranslational modifications. PCR (primer

XX generation reaction) is a reaction that is designed to produce at least

XX one nucleic acid primer from a PCR initiation sequence of an RCR (rolling

XX circle reaction) product and the resulting primer is designed to prime to

XX a circular nucleic acid probe and initiate RCR. On the other hand, RCR is

XX designed to produce concatenated sequence copies of the circular probe,

CC in which the resulting product contains at least one PCR initiation  
 CC sequence in every repeat sequence just like the initial reaction signal.  
 CC The first and second nucleic acid primers are generated by one of  
 CC nuclease-based cleavage reaction, strand displacement amplification,  
 CC cleavage-initiated isothermal amplification, three-way junction  
 CC isothermal amplification, three-way junction rolling circle reaction,  
 CC binding assay using a nucleic acid labeled recognition agent and  
 CC proximity assay. The method of nucleic acid detection using the present  
 CC invention is useful for in vitro diagnostics and in pathogen detection.  
 CC The nucleotide sequence presented here is the target nucleic acid used in  
 CC PG-RCA using ribbon probe.

XX Sequence 24 BP; 5 A; 5 C; 6 G; 5 T; 3 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 24;

Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGCCGT 20

Db 1 CCAGTTGAAGTTGCCGT 17

#### RESULT 6

AEJ10483/C

ID AEJ10483 standard; DNA; 42 BP.

XX AC AEJ10483;

DT 07-SEP-2006 (first entry)

XX Circularizable lock probe used for ribbon probe synthesis.

XX DNA detection; microorganism detection; SNP detection;  
 KW epigenetic modification; diagnostic; RNA detection; DNA amplification;  
 KW DNA methylation; gene amplification; primer extension; probe; PCR;  
 KW circular; ss; DNA-RNA hybrid.

XX Synthetic.

XX Key Location/Qualifiers

FT misc\_RNA 16..19

FT /\*tag= a

XX WO2006074162-A2.

XX 13-JUL-2006.

PD 04-JAN-2006; 2006WO-US000086.

PP 04-JAN-2005; 2005US-0641255P.

PR 14-JUL-2005; 2005US-0699340P.

XX (HITB ) HITACHI CHEM CO LTD.

PA (HITB ) HITACHI CHEM RES CENT INC.

XX Murakami T;

PI WPI; 2006-513365/52.

DR Amplifying nucleic acid, by combining a nucleic acid primer with a

XX polymerase and a circular nucleic acid probe, and producing a repeat of a

XX sequence copy of the circular nucleic acid probe.

XX Example 5; SEQ ID NO 15; 34pp; English.

XX The present invention discloses a method of amplifying nucleic acid using

XX primers and probes by rolling circle amplification method. The present

XX invention comprises primer generation ? rolling circle amplification (PG-

XX RCA) in which a ribbon probe is involved, allows the single step

XX detection of nucleic acid sequences such as DNA and RNA sensitively and

XX rapidly. This technology is easily applicable to detection of other

XX biomolecules such as DNA methylation, single nucleotide polymorphism

(SNP), protein and posttranslational modifications. PCR (primer generation reaction) is a reaction that is designed to produce at least one nucleic acid primer from a PCR initiation sequence of an RCR (rolling circle reaction) product and the resulting primer is designed to prime to a circular nucleic acid probe and initiate RCR. On the other hand, RCR is designed to produce concatenated sequence copies of the circular probe, in which the resulting product contains at least one PCR initiation sequence in every repeat sequence just like the initial reaction signal. The first and second nucleic acid primers are generated by one of nuclease-based cleavage reaction, strand displacement amplification, cleavage-initiated isothermal amplification, three-way junction isothermal amplification, three-way junction rolling circle reaction, binding assay using a nucleic acid labeled recognition agent and proximity assay. The method of nucleic acid detection using the present invention is useful for in vitro diagnostics and in pathogen detection. The nucleotide sequence presented here is the circularizable lock probe used for ribbon probe synthesis.

XX Sequence 42 BP; 12 A; 10 C; 12 G; 7 T; 1 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 42;  
Best Local Similarity 100.0%; Pred. No. 7.6;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGCCGT 20  
|||||

Db 35 CCAGTTGAAGTTGCCGT 19  
|||||

RESULT 7  
AEJ10476/c  
ID AEJ10476 standard; DNA; 44 BP.  
AC AEJ10476;  
XX  
XX  
DT 07-SEP-2006 (first entry)  
XX  
XX Circularizable probe for nuclease-based cleavage reaction PG-RCA.  
DE  
XX DNA detection; microorganism detection; SNP detection;  
KW epigenetic modification; diagnostic; RNA detection; DNA amplification;  
KW DNA methylation; gene amplification; primer extension; probe; PCR;  
KW circular; ss.  
XX  
OS Synthetic.  
XX  
XX WO2006074162-A2.  
XX  
PD 13-JUL-2006.  
XX  
XX 04-JAN-2006; 2006WO-US000086.  
XX  
XX 04-JAN-2005; 2005US-0641255P.  
PR 14-JUL-2005; 2005US-0699340P.  
XX  
XX (HITB ) HITACHI CHEM CO LTD.  
PA (HITB ) HITACHI CHEM RES CENT INC.  
XX  
XX Murakami T;  
PI  
XX  
XX WPI; 2006-513365/52.  
DR  
XX Amplifying nucleic acid, by combining a nucleic acid primer with a  
PT polymerase and a circular nucleic acid probe, and producing a repeat of a  
PT sequence copy of the circular nucleic acid probe.  
XX  
XX Example 3; SEQ ID NO 8; 34pp; English.  
XX  
XX The present invention discloses a method of amplifying nucleic acid using  
CC primers and probes by rolling circle amplification method. The present  
CC invention comprises primer generation ? rolling circle amplification (PG-  
CC RCA) in which a ribbon probe is involved, allows the single step  
CC detection of nucleic acid sequences such as DNA and RNA sensitively and

CC rapidly. This technology is easily applicable to detection of other biomolecules such as DNA methylation, single nucleotide polymorphism (SNP), protein and posttranslational modifications. PCR (primer generation reaction) is a reaction that is designed to produce at least one nucleic acid primer from a PCR initiation sequence of an RCR (rolling circle reaction) product and the resulting primer is designed to prime to a circular nucleic acid probe and initiate RCR. On the other hand, RCR is designed to produce concatenated sequence copies of the circular probe, in which the resulting product contains at least one PCR initiation sequence in every repeat sequence just like the initial reaction signal. The first and second nucleic acid primers are generated by one of nuclease-based cleavage reaction, strand displacement amplification, cleavage-initiated isothermal amplification, three-way junction isothermal amplification, three-way junction rolling circle reaction, binding assay using a nucleic acid labeled recognition agent and proximity assay. The method of nucleic acid detection using the present invention is useful for in vitro diagnostics and in pathogen detection. The nucleotide sequence presented here is the circularizable probe for nuclease-based cleavage reaction PG-RCA.

XX Sequence 44 BP; 10 A; 13 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7.6;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGCCGT 20  
|||||

Db 28 CCAGTTGAAGTTGCCGT 12  
|||||

RESULT 8  
AEJ10482/c  
ID AEJ10482 standard; DNA; 44 BP.  
XX  
XX AEJ10482;  
XX  
XX 07-SEP-2006 (first entry)  
XX  
XX Circularizable probe used for ribbon probe synthesis.  
DE  
XX DNA detection; microorganism detection; SNP detection;  
KW epigenetic modification; diagnostic; RNA detection; DNA amplification;  
KW DNA methylation; gene amplification; primer extension; probe; PCR;  
KW circular; ss.  
XX  
OS Synthetic.  
XX  
XX WO2006074162-A2.  
XX  
PD 13-JUL-2006.  
XX  
XX 04-JAN-2006; 2006WO-US000086.  
XX  
XX 04-JAN-2005; 2005US-0641255P.  
PR 14-JUL-2005; 2005US-0699340P.  
XX  
XX (HITB ) HITACHI CHEM CO LTD.  
PA (HITB ) HITACHI CHEM RES CENT INC.  
XX  
XX Murakami T;  
PI  
XX  
XX WPI; 2006-513365/52.  
DR  
XX Amplifying nucleic acid, by combining a nucleic acid primer with a  
PT polymerase and a circular nucleic acid probe, and producing a repeat of a  
PT sequence copy of the circular nucleic acid probe.  
XX  
XX Example 5; SEQ ID NO 14; 34pp; English.  
XX  
XX The present invention discloses a method of amplifying nucleic acid using  
CC primers and probes by rolling circle amplification method. The present  
CC invention comprises primer generation ? rolling circle amplification (PG-  
CC RCA) in which a ribbon probe is involved, allows the single step  
CC detection of nucleic acid sequences such as DNA and RNA sensitively and

CC RCA) in which a ribbon probe is involved, allows the single step  
 CC detection of nucleic acid sequences such as DNA and RNA sensitively and  
 CC rapidly. This technology is easily applicable to detection of other  
 CC biomolecules such as DNA methylation, single nucleotide polymorphism  
 CC (SNP), protein and posttranslational modifications. PCR (primer  
 CC generation reaction) is a reaction that is designed to produce at least  
 CC one nucleic acid primer from a PCR initiation sequence of an RCR (rolling  
 CC circle reaction) product and the resulting primer is designed to prime to  
 CC a circular nucleic acid probe and initiate RCR. On the other hand, RCR is  
 CC designed to produce concatenated sequence copies of the circular probe,  
 CC in which the resulting product contains at least one PCR initiation  
 CC sequence in every repeat sequence just like the initial reaction signal.  
 CC The first and second nucleic acid primers are generated by one of  
 CC nuclease-based cleavage reaction, strand displacement amplification,  
 CC cleavage-initiated isothermal amplification, three-way junction  
 CC isothermal amplification, three-way junction rolling circle reaction,  
 CC binding assay using a nucleic acid labeled recognition agent and  
 CC proximity assay. The method of nucleic acid detection using the present  
 CC invention is useful for in vitro diagnostics and in pathogen detection.  
 CC The nucleotide sequence presented here is the circularizable probe used  
 CC for ribbon probe synthesis.

XX SQ Sequence 44 BP; 10 A; 13 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 44;

Best Local Similarity 100.0%; Pred. No. 7.6; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0

Qy 4 CCAGTTGAAGTTGCCGT 20

Db 28 CCAGTTGAAGTTGCCGT 12

RESULT 9

AEJ10475/C  
 ID AEJ10475 standard; DNA; 45 BP.

AC AEJ10475;

XX 07-SEP-2005 (first entry)

XX PGR probe for nuclease-based cleavage reaction PG-RCA.

XX DNA detection; microorganism detection; SNP detection;  
 KW epigenetic modification; diagnostic; RNA detection; DNA amplification;  
 KW DNA methylation; gene amplification; primer extension; probe; PCR;  
 KW Primer; DNA-RNA hybrid; ss.

XX Synthetic.

XX Key Location/Qualifiers

EH misc\_RNA

ET 23..26 /\*tag= a

FT 43..45 /\*tag= b

FT 43..45 /\*tag= c

ET /mod\_base= 2'-O-methyluridine

XX WO2006074162-A2.

XX 13-JUL-2006.

XX 04-JAN-2006; 2006WO-US000086.

XX 04-JAN-2005; 2005US-0641255P.

XX 14-JUL-2005; 2005US-0699340P.

XX (HLTB ) HITACHI CHEM CO LTD.

XX (HLTB ) HITACHI CHEM RES CENT INC.

XX Murakami T;

XX

XX

XX

XX

XX

XX

XX

XX

DR WPI; 2006-513365/52.

XX Amplifying nucleic acid, by combining a nucleic acid primer with a  
 PT polymerase and a circular nucleic acid probe, and producing a repeat of a  
 PT sequence copy of the circular nucleic acid probe.

XX Example 3; SEQ ID NO 7; 34pp; English.

XX The present invention discloses a method of amplifying nucleic acid using  
 CC primers and probes by rolling circle amplification method. The present  
 CC invention comprises primer generation ? rolling circle amplification (PG-  
 CC RCA) in which a ribbon probe is involved, allows the single step  
 CC detection of nucleic acid sequences such as DNA and RNA sensitively and  
 CC rapidly. This technology is easily applicable to detection of other  
 CC biomolecules such as DNA methylation, single nucleotide polymorphism  
 CC (SNP), protein and posttranslational modifications. PCR (primer  
 CC generation reaction) is a reaction that is designed to produce at least  
 CC one nucleic acid primer from a PCR initiation sequence of an RCR (rolling  
 CC circle reaction) product and the resulting primer is designed to prime to  
 CC a circular nucleic acid probe and initiate RCR. On the other hand, RCR is  
 CC designed to produce concatenated sequence copies of the circular probe,  
 CC in which the resulting product contains at least one PCR initiation  
 CC sequence in every repeat sequence just like the initial reaction signal.  
 CC The first and second nucleic acid primers are generated by one of  
 CC nuclease-based cleavage reaction, strand displacement amplification,  
 CC cleavage-initiated isothermal amplification, three-way junction  
 CC isothermal amplification, three-way junction rolling circle reaction,  
 CC binding assay using a nucleic acid labeled recognition agent and  
 CC proximity assay. The method of nucleic acid detection using the present  
 CC invention is useful for in vitro diagnostics and in pathogen detection.  
 CC The nucleotide sequence presented here is the PGR probe for nuclease-  
 CC based cleavage reaction PG-RCA.

XX SQ Sequence 45 BP; 12 A; 10 C; 12 G; 7 T; 4 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 45;

Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGCCGT 20

Db 42 CCAGTTGAAGTTGCCGT 26

RESULT 10

ABX13068

ID ABX13068 standard; DNA; 20 BP.

XX AC ABX13068;

XX 29-MAY-2003 (first entry)

XX Human bax PCR primer #2.

XX Human; insulin-like growth factor binding protein 5; IGFBP-5; primer; ss;  
 KW cytosstatic; apoptosis; cancer; breast; prostate; ovary; lung; colon; PCR;  
 KW bax.

XX Homo sapiens.

XX WO2003006029-A1.

XX 23-JAN-2003.

XX 15-JUL-2002; 2002WO-AU000936.

XX 13-JUL-2001; 2001AU-00006331.

XX (UNSY ) UNIV SYDNEY.

XX Baxter RC, Butt AJ;

XX WPI; 2003-221646/21.

XX

XX

XX

XX

XX Inducing apoptosis in cancer cell, useful for treating cancer, e.g.  
 PT breast or prostate cancer comprises increasing the expression of insulin-  
 PT like growth factor binding protein-5 (IGFBP-5) by the cell to an  
 PT apoptosis-inducing amount.

XX Example; Page 29; 65pp; English.

XX The invention relates to a method for inducing apoptosis in a cancer cell  
 CC comprising increasing the expression of insulin-like growth factor  
 CC binding protein 5 (IGFBP-5) by the cell to an apoptosis-inducing amount.  
 CC The invention also relates to a method of sensitising a cancer cell to  
 CC stimuli that induce apoptosis by increasing the expression of IGFBP-5 by  
 CC the cell, a method of killing a cancer cell by sensitising the cell to  
 CC stimuli that induce apoptosis and simultaneously exposing the cell to  
 CC apoptosis-inducing stimuli, or exposing the cell to apoptosis-inducing  
 CC stimuli and simultaneously or subsequently increasing the expression of  
 CC IGFBP-5 by the cell to an apoptosis-inducing amount. The methods are  
 CC useful for treating cancer, such as breast, prostate, ovarian, lung or  
 CC colon cancer, by inducing apoptosis or killing cancer cells. This  
 CC sequence represents a bax PCR primer used in the method of the invention

XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 28; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTCGGT 20

Db 1 CAGTTGAAGTTCGGT 16

RESULT 11

ADA20946

ID ADA20946 standard; DNA; 20 BP.

XX ADA20946;

XX 20-NOV-2003 (first entry)

XX Mouse BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:119.

XX BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;  
 KW anticonvulsant; ophthalmological; antidiabetic; virucide;  
 KW antisense therapy; BAX antagonist; BAX inhibitor;  
 KW familial amyotrophic lateral sclerosis; Alzheimer's disease;  
 KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;  
 KW diabetes-associated ocular disorder; scrapie infection;  
 KW aberrant apoptosis; mouse; phosphorothioate; ss.

XX Synthetic.

OS Mus musculus.

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /tag= b

FT /mod\_base= OTHER

FT /note= "phosphorothioate linkages, and all cytidine

FT residues are 5-methylcytidines"

FT modified\_base 1..5

FT /tag= a

FT /mod\_base= OTHER

FT /note= "2'-O-methoxyethyls"

FT modified\_base 16..20

FT /tag= c

FT /mod\_base= OTHER

FT /note= "2'-O-methoxyethyls"

XX WO2003008543-A2.

XX 30-JAN-2003.

XX

PF 13-JUL-2002; 2002WO-US022417.

XX

PR 17-JUL-2001; 2001US-00908147.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Zhang H, Watt AT;

XX

DR WPI; 2003-239321/23.

XX

PT New antisense compounds, useful for modulating the expression of BCL2-  
 PT associated X (BAX) protein or for treating a disease or condition  
 PT associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease  
 PT or Alzheimer's disease.

XX Claim 3; Page 93; 139pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length  
 CC targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)  
 CC protein, where the compound specifically hybridises with the nucleic acid  
 CC molecule encoding BAX protein and inhibits the expression of BAX protein.  
 CC The compound specifically hybridises with at least 8-nucleobase portion  
 CC of an active site on a nucleic acid molecule encoding BAX protein. Also  
 CC described: (1) a composition comprising (I) and a pharmaceutical carrier  
 CC or diluent; (2) inhibiting the expression of BAX protein in cells or  
 CC tissues comprising contacting the cells or tissues with (I); and (3)  
 CC treating an animal having a disease or condition associated with BAX  
 CC protein comprising administering to the animal (I) so that expression of  
 CC BAX protein is inhibited. (I) has neurotropic, neuroprotective,  
 CC antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and  
 CC virucide activities, and can be used in antisense therapy, and as a BAX  
 CC antagonist. The antisense compounds (I) are useful for modulating the  
 CC expression of BAX protein, and for treating a disease or condition  
 CC associated with BAX protein, e.g. familial amyotrophic lateral  
 CC sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,  
 CC cartilage-hair hyperplasia, diabetes-associated ocular disorders or  
 CC scrapie infection, or a condition that arises from aberrant apoptosis.  
 CC The compounds are useful as research reagents and in diagnostics. The  
 CC present sequence represents a mouse BAX chimeric phosphorothioate  
 CC oligonucleotide, which is used in an example from the present invention.

XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGTTCGC 18

Db 1 CCCAGTTGAAGTTCGC 16

RESULT 12

AED12216

ID AED12216 standard; DNA; 20 BP.

XX

AC AED12216;

XX

DT 01-DEC-2005 (first entry)

XX

DE Bax (human) RT-PCR primer SEQ ID 16.

XX

KW Drug screening; apoptosis; protein interaction; Bax; Cytostatic;

KW Neuroprotective; cancer; neurodegenerative disease; ss; RT-PCR;

KW reverse transcriptase PCR; primer.

XX

OS Homo sapiens.

XX

PN WO2005093082-A1.

XX

PD 06-OCT-2005.

XX

PF 23-MAR-2005; 2005WO-JP005247.

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XX 26-MAR-2004; 2004JP-00093266.
PR 14-JUN-2004; 2004JP-00176107.
XX
XX (HISM ) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
XX
XX Nakagawara A, Ozaki T;
XX WPI; 2005-713863/73.
XX
XX Screening compound capable of stimulating or inhibiting apoptosis,
PT involves judging compound capable of intensifying interaction between p73
PT and IKK-alpha as compound capable of stimulating or inhibiting apoptosis.
XX
XX Example; SEQ ID NO 16; 79pp; Japanese.
XX
XX The invention relates to screening (M1) a compound capable of stimulating
CC or inhibiting apoptosis, comprising identifying a compound capable of
CC modulating the interaction between p73 and IKK-alpha (IkappaB kinase) as
CC a compound capable of stimulating or inhibiting apoptosis. The method
CC comprise culturing a cell that expresses p73 and IKK-alpha in the
CC presence or absence of test compound, measuring an interaction between
CC p73 and IKK-alpha in each cultured cell and judging a compound as being
CC capable of stimulating or inhibiting apoptosis, when an interaction
CC between p73 and IKK-alpha in the cell cultured in the presence of test
CC compound, is stronger or weaker, in comparison to cell cultured in the
CC absence of test compound, respectively. Also included are an apoptosis
CC stimulator comprising AED12224 (human IKK-alpha, or a nucleic acid that
CC encodes human IKK-alpha) and an apoptosis inhibitor comprising human IKK-
CC alpha K44A mutant (AED12225) or human ubiquitin fusion degradation
CC protein-2a (AED12226). The method is useful for screening a compound
CC capable of stimulating or inhibiting apoptosis utilized for treating
CC cancer or neurodegenerative diseases. The present sequence is an RT-PCR
CC primer for a non-IKK mRNA (i.e. is either a control or is for an IKK
CC binding protein).
XX
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 80.0%; Score 16; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. NO. 28;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
DB 1 CAGTTGAAGTTGCCGT 16

RESULT 13
AEJ97326
ID AEJ97326 standard; DNA; 20 BP.
XX
XX AEJ97326;
AC
XX
XX 02-NOV-2006 (first entry)
DT
XX
XX RT-PCR primer BAX reverse, SEQ ID 8.
DE
XX
XX Therapeutic; apoptosis inhibition; apoptosis stimulation; neoplasm;
KW cancer; neurodegenerative disease; neurological disorder; RT-PCR; primer;
KW ss.
XX
XX Homo sapiens.
OS
XX
XX JP2006223265-A.
PN
XX
XX 31-AUG-2006.
PD
XX
XX 21-FEB-2005; 2005JP-00044554.
PF
XX
XX 21-FEB-2005; 2005JP-00044554.
PR
XX
XX (HISM ) HISAMITSU PHARM CO LTD.
PA

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PA (CHIB-) CHIBA PREFECTURE.
XX
XX Nakagawara A, Ozaki T;
XX WPI; 2006-590511/61.
XX
XX Screening compound capable of promoting or suppressing apoptosis, for
PT treating cancer or neurodegenerative disease, involves determining
PT whether compound inhibits or enhances interaction of p53 and NFBD1.
XX
XX Example; SEQ ID NO 8; 21pp; Japanese.
XX
XX The invention relates to the screening of a compound capable of promoting
CC or suppressing apoptosis. The method comprises determining whether a
CC compound inhibits or enhances the interaction of p53 and NFBD1 (nuclear
CC factor with BRC1 domains protein 1), or culturing a cell expressing p53
CC and NFBD1 in the presence and in the absence of a test compound and
CC measuring the interaction of p53 and NFBD1 in a cultured cell. Further,
CC disclosed is an apoptosis inhibitor with p53 binding activity having an
CC amino acid sequence as given in AEJ97331. The method is useful for
CC screening a compound that promotes or suppresses apoptosis and is useful
CC as a therapeutic agent for cancer and neurodegenerative disorders. The
CC current sequence represents an RT-PCR primer used in an exemplification
CC of the invention.
XX
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 80.0%; Score 16; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. NO. 28;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
DB 1 CAGTTGAAGTTGCCGT 16

RESULT 14
AEK58344
ID AEK58344 standard; DNA; 20 BP.
XX
XX AEK58344;
AC
XX
XX 16-NOV-2006 (first entry)
DT
XX
XX Interferon-related gene specific PCR primer, SEQ ID NO:21.
DE
XX
XX screening; gene expression; hepatitis C virus infection;
KW antiinflammatory; hepatotropic; virucide; gastrointestinal disease;
KW infection; diagnostic; diagnosis; liver cirrhosis; inflammation;
KW microarray; DNA amplification; therapeutic; ss; primer; PCR; interferon.
XX
XX Homo sapiens.
OS
XX
XX WO2006085407-A1.
PN
XX
XX 17-AUG-2006.
PD
XX
XX 30-SEP-2005; 2005WO-JP018573.
PF
XX
XX 09-FEB-2005; 2005JP-00033707.
PR
XX
XX (UYNI-) UNIV NIPPON.
PA
XX
XX Esami M, Takayama T;
PI
XX
XX WPI; 2006-680124/70.
DR
XX
XX Screening gene whose expression is increased in high/low hepatitis C
PT virus (HCV) tissue, involves selecting gene based on its expression level
PT in low and high virus group tissues being selected based on HCV 18S rRNA
PT analysis.
XX
XX Example 1; SEQ ID NO 21; 75pp; Japanese.
PS

```

XX The new invention relates to screening a gene whose expression is  
CC increased in high hepatitis C virus (HCV) group tissue or low HCV group  
CC tissue. The method involves selecting liver tissue whose value is  
CC obtained by dividing copy number of HCV per 50 ng of liver tissue-derived  
CC cDNA by the value of 18S rRNA is not more than 300 units as low virus  
CC group tissue and not more than 3000 units as high virus group tissue,  
CC measuring gene expression level in tissues, and selecting gene whose  
CC expression is increased in high/low virus group tissue more than low/high  
CC virus group tissue. Also described is a diagnostic of diseases relevant  
CC to viral load, comprising (a) gene (e.g. OASL, EHF, CXCL6, IRS2, MAP1B  
CC and CXCL10) with a sequence of one of SEQ ID No. 54-131, where the  
CC expression of the gene enhances in high virus group, (b) gene (e.g.  
CC FLJ4615, 28S rRNA, ENCL, RAPHI, BAGE and PSMA8) comprising a sequence of  
CC one of SEQ ID No. 132-170, where the expression of the gene enhances in  
CC low virus group, (c) one of gene (e.g. HUA-DQAL, TMRPS2, SPEC2, SNA12,  
CC IFI44, LEPK and FNB1) of CHH gene cluster comprising a sequence of SEQ  
CC ID No. 171-237, where the expression of the gene enhances in high virus  
CC group of chronic hepatitis, (d) one of gene (e.g. FLJ46154, KCNN2, CRP,  
CC LOC134145 and HMG2) of CHL gene cluster comprising a sequence of SEQ ID  
CC No. 238-258, where the expression of the gene enhances in low virus group  
CC of chronic hepatitis, (e) one of gene (e.g. SDS, GLP2, KLF6, ZDHHC11,  
CC GADD45D, MX1 and BC13) of LCH gene cluster comprising a sequence of one  
CC of SEQ ID No. 259-285, where the expression of the gene enhances in high  
CC virus group of liver cirrhosis, or (f) one of gene (e.g. MND4, CLECSF12,  
CC SUC8A1, PST, API52, LARS and TBC1D1) of LCL gene cluster comprising a  
CC sequence of one of SEQ ID No. 286-302, where the expression of the gene  
CC enhances in low virus group of liver cirrhosis. The measurement of  
CC expression is carried out using microarray and/or real-time PCR. The  
CC method is useful for screening a gene whose expression is increased in a  
CC high virus group tissue containing a large amount of HCV or in a low  
CC virus group tissue containing small amount of HCV, for development of  
CC therapeutic agent of HCV. This sequence is a primer for PCR amplification  
CC of an interferon-related gene, useful in the new method of the invention.  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 19; Length 20;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTCGCGT 20  
Db 1 CAGTTGAAGTTCGCGT 16

## RESULT 15

AEH24548/c  
ID AEH24548 standard; DNA; 22 BP.

XX AEH24548;

XX 29-JUN-2006 (first entry)

XX BAX gene forward PCR primer.

XX ss; PCR; primer; drug metabolism; cancer; cytostatic; neoplasm;  
KW immune inhibition; apoptosis stimulation; RNA quantitation; BAX.

XX Homo sapiens.

XX WO2006045053-A2.

XX 27-APR-2006.

XX 20-OCT-2005; 2005WO-US037925.

XX 20-OCT-2004; 2004US-0620603P.

XX 16-FEB-2005; 2005US-0653557P.

XX 08-JUN-2005; 2005US-0688741P.

XX (HITB ) HITACHI CHEM CO LTD.

XX (HITB ) HITACHI CHEM RES CENT INC.

XX Mitsuhaashi M;  
PI  
XX  
DR WPI; 2006-332057/34.

XX Measuring a patient's responsiveness to a drug comprises exposing whole  
PT blood of the patient to the drug for 7 hours or less, and measuring the  
PT amount of an mRNA associated with an effect of the drug in blood cells.  
XX  
XX Disclosure; SEQ ID NO 39; 74pp; English.

XX The invention relates to a method of measuring a patient's responsiveness  
CC to a which drug comprises exposing whole blood of the patient to the drug  
CC for 7 hours or less, and measuring the amount of an mRNA associated with  
CC an effect of the drug in blood cells. Preferably, the amount of the mRNA  
CC present in the blood cells is measured before the exposure, and the  
CC change in the amount of the mRNA is determined by comparing the amount of  
CC mRNA measured before exposure to the amount of mRNA measured after  
CC exposure. The method additionally comprises exposing whole blood of the  
CC patient to a control vehicle for 7 hours or less; after the exposure,  
CC measuring the amount of the mRNA associated with an effect of the drug in  
CC the blood cells exposed to the control vehicle; and identifying  
CC responsiveness to the drug includes comparing results of the measurement  
CC obtained after exposure to the control vehicle with results of the  
CC measurement obtained after exposure to the drug. The control vehicle is  
CC selected from phosphate-buffered saline and dimethyl sulfoxide. The mRNA  
CC is selected from mRNAs encoding the gene products of the Bcl-2/Bax gene  
CC family, Bax gene product, the BH3-only Bcl-2 gene family, ATP-binding  
CC cassette subfamilies A to G, and p21, PUMA and NOXA gene products. The  
CC method is useful for measuring a patient's responsiveness to a drug,  
CC which is useful in developing an optimized treatment protocol tailored to  
CC the specific patient. The method may be used for patients with conditions  
CC such as cancer or diseases which require immunosuppression. The present  
CC sequence represents BAX gene forward PCR primer. This gene was amplified  
CC in studies of drug induced apoptosis in tailored drug administration for  
CC leukemia and lymphoma.

XX Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 19; Length 22;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTCGCGT 20

Db 22 CAGTTGAAGTTCGCGT 7

Search completed: December 3, 2007, 16:22:19  
Job time : 1240 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:58:53 ; Search time 221 Seconds  
(without alignments)  
339.009 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagtgaggtgcgct 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 43

Minimum DB seq length: 12

Maximum DB seq length: 30

Post-processing: Minimum Score over Length 70%  
Listing first 1000 summaries

Database : Issued Patents NA:\*

- 1: /EMC\_Celerra\_SIDS2/ptodata/1/ina/1 COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS2/ptodata/1/ina/5 COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS2/ptodata/1/ina/6A COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS2/ptodata/1/ina/6B COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS2/ptodata/1/ina/7A COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS2/ptodata/1/ina/7B COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS2/ptodata/1/ina/H COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS2/ptodata/1/ina/PTUS\_COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS2/ptodata/1/ina/PP COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS2/ptodata/1/ina/RE COMB.seq:\*
- 11: /EMC\_Celerra\_SIDS2/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11.4	81.4	57.0	14	US-09-341-700A-857
C 2	12	80.0	60.0	15	US-08-584-040-8471
C 3	12	80.0	60.0	15	US-09-371-772B-4126
C 4	12	80.0	60.0	15	US-09-685-664B-4126
C 5	12	80.0	60.0	15	US-10-138-674B-4126
C 6	10.4	74.3	52.0	14	US-09-168-791-14
C 7	10.4	74.3	52.0	14	US-09-168-714-14
C 8	11.8	73.8	59.0	16	US-09-371-772B-5807
C 9	11.8	73.8	59.0	16	US-10-138-674B-5807
C 10	11	73.3	55.0	15	US-08-584-040-8496
C 11	11	73.3	55.0	15	US-09-371-772B-4150
C 12	11	73.3	55.0	15	US-09-685-664B-4150
C 13	11	73.3	55.0	15	US-10-138-674B-4150
C 14	8.8	73.3	44.0	12	US-08-441-887A-238
C 15	8.8	73.3	44.0	12	US-08-441-887A-239
C 16	8.8	73.3	44.0	12	US-09-417-455-22
C 17	8.8	73.3	44.0	12	US-09-348-942-22
C 18	8.8	73.3	44.0	12	US-09-457-626-22
C 19	8.8	73.3	44.0	12	US-09-576-008-22
C 20	8.8	73.3	44.0	12	US-08-510-521E-357
C 21	8.8	73.3	44.0	12	US-08-510-521E-358
C 22	8.8	73.3	44.0	12	US-10-070-588A-32
C 23	13.8	72.6	69.0	19	US-10-310-914B-801404

24	10	71.4	50.0	14	US-09-341-700A-858	Sequence 8
C 25	12.8	71.1	64.0	18	US-10-310-914B-1258144	Sequence 1
C 26	12	70.6	60.0	17	US-08-584-040-3879	Sequence 3
C 27	12	70.6	60.0	17	US-08-584-040-3880	Sequence 3
C 28	12	70.6	60.0	17	US-09-371-772B-1646	Sequence 1
C 29	12	70.6	60.0	17	US-09-371-772B-1647	Sequence 1
C 30	12	70.6	60.0	17	US-09-371-772B-6253	Sequence 6
C 31	12	70.6	60.0	17	US-09-371-772B-6254	Sequence 6
C 32	12	70.6	60.0	17	US-09-685-664B-1646	Sequence 1
C 33	12	70.6	60.0	17	US-09-685-664B-1647	Sequence 1
C 34	12	70.6	60.0	17	US-10-138-674B-1647	Sequence 1
C 35	12	70.6	60.0	17	US-10-138-674B-1647	Sequence 1
C 36	12	70.6	60.0	17	US-10-138-674B-6253	Sequence 6
C 37	12	70.6	60.0	17	US-10-138-674B-6254	Sequence 6
C 38	12	70.6	60.0	17	US-10-138-674B-8571	Sequence 8
C 39	13.4	70.5	67.0	19	US-10-310-914B-1191074	Sequence 1
C 40	8.4	70.0	42.0	12	US-08-401-512-16	Sequence 1
C 41	8.4	70.0	42.0	12	US-08-738-381-48	Sequence 4
C 42	8.4	70.0	42.0	12	US-10-078-958-50	Sequence 5
C 43	8.4	70.0	42.0	12	US-10-078-958-59	Sequence 5

ALIGNMENTS

RESULT 1  
US-09-341-700A-857  
; Sequence 857, Application US/09341700A  
; Patent No. 6972171  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Brysch, Wolfgang  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
; FILE REFERENCE: 10496/P63763USO  
; CURRENT APPLICATION NUMBER: US/09/341,700A  
; CURRENT FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: PCT/EP98/00497  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: EP 97 101 531.8  
; PRIOR FILING DATE: 1997-01-31  
; NUMBER OF SEQ ID NOS: 1764  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 857  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: antisense oligonucleotide  
US-09-341-700A-857

Query Match 57.0%; Score 11.4; DB 4; Length 14;  
Score over Length 81.4%;  
Best Local Similarity 92.3%; Pred. No. 5.4e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCG 19  
|||||||  
Db 2 GTTGAAGTTGCTG 14

RESULT 2  
US-08-584-040-8471/c  
; Sequence 8471, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS



;; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
;; TITLE OF INVENTION: GROWTH FACTOR  
;; NUMBER OF SEQUENCES: 8502  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; CITY: Suite 4700  
;; STATE: Los Angeles  
;; COUNTRY: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071-2066  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/584,040  
;; FILING DATE: January 11, 1996  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/005,974  
;; FILING DATE: October 26, 1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 218/064  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 8471:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-584-040-8471

Query Match 60.0%; Score 12; DB 3; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14  
Db 15 CCCAGTTGAAGT 4

## RESULT 3

US-09-371-772B-4126/c  
; Sequence 4126, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH800.876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4126  
; LENGTH: 15

;; TYPE: RNA  
;; ORGANISM: Mus sp.  
;; US-09-371-772B-4126  
  
Query Match 60.0%; Score 12; DB 3; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 CCCAGTTGAAGT 14  
Db 15 CCCAGTTGAAGT 4

## RESULT 4

US-09-685-664B-4126/c  
; Sequence 4126, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related  
; FILE REFERENCE: MBH800-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4126  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; US-09-685-664B-4126

Query Match 60.0%; Score 12; DB 3; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14  
Db 15 CCCAGTTGAAGT 4

## RESULT 5

US-10-138-674B-4126/c  
; Sequence 4126, Application US/10138674B  
; Patent No. 7034009  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH800-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674B  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4126  
; LENGTH: 15  
; TYPE: RNA





Db 2 GACCCAGAGUAGU 16

RESULT 10  
US-08-584-040-8496/c  
; Sequence 8496, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: Storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/584,040  
; FILING DATE: January 11, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/005,974  
; FILING DATE: October 26, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 218/064  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 8496:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-584-040-8496

Query Match 55.0%; Score 11; DB 3; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 8.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
Db 15 CCAGTTGAAGT 5

RESULT 11  
US-09-371-7728-4150/c  
; Sequence 4150, Application US/093717728  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Mus sp.  
US-09-371-7728-4150

Query Match 55.0%; Score 11; DB 3; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 8.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
Db 15 CCAGTTGAAGT 5

RESULT 12  
US-09-685-664B-4150/c  
; Sequence 4150, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-685-664B-4150

Query Match 55.0%; Score 11; DB 3; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 8.5e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
Db 15 CCAGTTGAAGT 5

RESULT 13  
US-10-138-674B-4150/c  
; Sequence 4150, Application US/10138674B  
; Patent No. 7034009  
; GENERAL INFORMATION:

```
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggan, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-4150

Query Match      55.0%; Score 11; DB 5; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CCAGTTGAAGT 14
      |||||
Db      15 CCAGTTGAAGT 5

RESULT 14
US-08-441-887A-238
; Sequence 238, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:

Query Match      44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 TGAAGTTGCCGT 20
      |||||
Db      1 TGCAGTTGCAGT 12

RESULT 15
US-08-441-887A-239
; Sequence 239, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; INFORMATION FOR SEQ ID NO: 239:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
US-08-441-887A-239

Query Match 44.0%; Score 8.8; DB 2; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.7e+05;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17  
|||||  
Db 1 ATTGGAGTTGC 12

## RESULT 16

US-09-417-455-22  
; Sequence 22, Application US/09417455  
; Patent No. 6294655  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF  
; FILE REFERENCE: 28110/36328  
; CURRENT APPLICATION NUMBER: US/09/417,455  
; CURRENT FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: US 09/348,942  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: PCT/US99/04291  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: US 09/287,210  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: US 09/251,370  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: US 09/229,591  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 09/127,698  
; PRIOR FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: US 09/099,818  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: US 09/082,364  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 09/079,909  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 09/055,010  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Exon  
US-09-417-455-22

Query Match 44.0%; Score 8.8; DB 3; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 9.7e+05;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13

|||||

Db 1 CCACAGGTGAAG 12

|||||

RESULT 17

US-09-348-942-22

; Sequence 22, Application US/09348942

; Patent No. 6337072

; GENERAL INFORMATION:

; APPLICANT: John Ford

; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF

; FILE REFERENCE: 28110/35801

; CURRENT APPLICATION NUMBER: US/09/348,942

; CURRENT FILING DATE: 1999-07-07

; QUERY MATCH: 44.0%; Score 8.8; DB 3; Length 12;

; Score over Length 73.3%;

; Best Local Similarity 83.3%; Pred. No. 9.7e+05;

; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

; QY 2 CCCAGTTGAAG 13

|||||

; Db 1 CCACAGGTGAAG 12

|||||

RESULT 18

US-09-457-626-22

; Sequence 22, Application US/09457626

; Patent No. 6426191

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Pace, Ann

; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF

; FILE REFERENCE: 28110/36010

; CURRENT APPLICATION NUMBER: US/09/457,626

; CURRENT FILING DATE: 1999-12-08

; PRIOR APPLICATION NUMBER: US 09/417,455

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: US 09/348,942

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: PCT/US99/04291

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: US 09/287,210

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: US 09/251,370

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: US 09/229,591

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 09/127,698

; PRIOR FILING DATE: 1998-07-31

; PRIOR APPLICATION NUMBER: US 09/099,818

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 09/082,364

; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: US 09/079,909

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: US 09/055,010

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 22

; LENGTH: 12

; TYPE: DNA

; ORGANISM: Exon

US-09-417-455-22

```
; TYPE: DNA
; ORGANISM: Exon
US-09-457-626-22

Query Match      44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
   |||||
Db 1 CCACAGGTGAAG 12

RESULT 19
US-09-576-008-22
; Sequence 22, Application US/09576008
; Patent No. 6541623
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice Suk-Yue
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36456
; CURRENT APPLICATION NUMBER: US/09/576,008
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/523,552
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/457,626
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: - US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Exon
US-09-576-008-22

Query Match      44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
   |||||
Db 1 CCACAGGTGAAG 12

RESULT 20
US-08-510-521E-357
; Sequence 357, Application US/08510521E
```

```
; Patent No. 7115364
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; Cronin, Maureen T.
; Fodor, Stephen P.A.
; Gingeras, Thomas R.
; Huang, Xiaohua C.
; Hubbell, Earl A.
; Lipshutz, Robert J.
; Lobban, Peter E.
; Morris, Macdonald S.
; Garrett Miyada, Charles
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; NUMBER OF SEQUENCES: 585
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: 2 Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/510,521E
; FILING DATE: 02-Aug-1995
; CLASSIFICATION: <Unknown>
; APPLICATION DATA:
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 357:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
; SEQUENCE DESCRIPTION: SEQ ID NO: 357:
US-08-510-521E-357

Query Match      44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.7e+05;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
   |||||
Db 1 TGGAGTTGCAGT 12

RESULT 21
US-08-510-521E-358
; Sequence 358, Application US/08510521E
; Patent No. 7115364
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; Cronin, Maureen T.
; Fodor, Stephen P.A.
```

/ Gingeras, Thomas R.  
/ Huang, Xiaohua C.  
/ Hubbell, Earl A.  
/ Lipshutz, Robert J.  
/ Lobban, Peter E.  
/ Garrett Miyada, Charles  
/ Morris, Macdonald S.  
/ TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
/ Biological Chips  
/ NUMBER OF SEQUENCES: 585  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: 2 Embarcadero Center, Eighth Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA: US/08/510,521E  
/ APPLICATION NUMBER: US/08/510,521E  
/ FILING DATE: 02-Aug-1995  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US94/12305  
/ FILING DATE: 26-OCT-1994  
/ APPLICATION NUMBER: US 08/284,064  
/ FILING DATE: 02-AUG-1994  
/ APPLICATION NUMBER: US 08/143,312  
/ FILING DATE: 26-OCT-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Liebeschultz, Joe  
/ REGISTRATION NUMBER: 37,505  
/ REFERENCE/DOCKET NUMBER: 018547-004120US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 415-576-0200  
/ TELEFAX: 415-576-0300  
/ INFORMATION FOR SEQ ID NO: 358:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 12 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (probe)  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 358:  
US-08-510-521E-358  
  
Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.7e+05;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 AGTTGAAGTTGC 17  
Db 1 ATTGGAGTTGC 12  
  
RESULT 22  
US-10-070-588A-32  
/ Sequence 32, Application US/10070588A  
/ Patent No. 7122652  
/ GENERAL INFORMATION:  
/ APPLICANT: EPIDAUROS AG  
/ TITLE OF INVENTION: Polymorphisms in the human hpxr gene and their use in  
/ diagnostic and therapeutic applications  
/ FILE REFERENCE: D 2145 PCT-2  
/ CURRENT APPLICATION NUMBER: US/10/070,588A  
/ PRIOR FILING DATE: 2002-03-08  
/ PRIOR APPLICATION NUMBER: PCT/EP00/08827  
/ PRIOR FILING DATE: 2000-09-08

/ NUMBER OF SEQ ID NOS: 185  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 32  
/ LENGTH: 12  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: variant of human pregnane X  
/ OTHER INFORMATION: receptor (hpxr) gene  
US-10-070-588A-32  
  
Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 9.7e+05;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 CCCAGTTGAAG 13  
Db 1 CCCAGGTGAGG 12  
  
RESULT 23  
US-10-310-914B-801404/C  
/ Sequence 801404, Application US/10310914B  
/ Patent No. 7250496  
/ GENERAL INFORMATION:  
/ APPLICANT: Bentwich, Isaac  
/ APPLICANT: Shiler, Kvazat  
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
/ uses thereof  
/ FILE REFERENCE: 06087.0200.CPUS01  
/ CURRENT APPLICATION NUMBER: US/10/310,914B  
/ CURRENT FILING DATE: 2002-12-06  
/ NUMBER OF SEQ ID NOS: 1388411  
/ SOFTWARE: PatentIn version 3.3  
/ SEQ ID NO 801404  
/ LENGTH: 19  
/ TYPE: RNA  
/ ORGANISM: Human  
US-10-310-914B-801404  
  
Query Match 69.0%; Score 13.8; DB 6; Length 19;  
Score over Length 72.6%;  
Best Local Similarity 88.2%; Pred. No. 3.8e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 CCCAGTTGAAGTTGCC 18  
Db 17 CCACATTTGAAGTTGCC 1  
  
RESULT 24  
US-09-341-700A-858  
/ Sequence 858, Application US/09341700A  
/ Patent No. 6972171  
/ GENERAL INFORMATION:  
/ APPLICANT: Schlengersien, Karl-Hermann  
/ APPLICANT: Brysch, Wolfgang  
/ TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
/ FILE REFERENCE: 10496/P63763USO  
/ CURRENT APPLICATION NUMBER: US/09/341,700A  
/ CURRENT FILING DATE: 1999-09-24  
/ PRIOR APPLICATION NUMBER: PCT/EP98/00497  
/ PRIOR FILING DATE: 1998-01-30  
/ PRIOR APPLICATION NUMBER: EP 97 101 531.8  
/ PRIOR FILING DATE: 1997-01-31  
/ NUMBER OF SEQ ID NOS: 1764  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 858  
/ LENGTH: 14  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: antisense oligonucleotide  
US-09-341-700A-858

Query Match 50.0%; Score 10; DB 4; Length 14;  
Score over Length 71.4%;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
|||||  
Db 5 GTTGAAGTTG 14

## RESULT 25

US-10-310-914B-1258144/c  
Sequence 1258144, Application US/10310914B  
Patent No. 7250496  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kvuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914B  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388411  
SOFTWARE: Patent in version 3.3  
SEQ ID NO 1258144  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914B-1258144

Query Match 64.0%; Score 12.8; DB 6; Length 18;  
Score over Length 71.1%;  
Best Local Similarity 87.5%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCCT 20  
|||||  
Db 17 CAGTTGAAGTCCACT 2

## RESULT 26

US-08-584-040-3879/c  
Sequence 3879, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 3879:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-3879

Query Match 60.0%; Score 12; DB 3; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
Db 17 CCCAGTTGAAGT 6

## RESULT 27

US-08-584-040-3880/c  
Sequence 3880, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 3880:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-584-040-3880

Query Match 60.0%; Score 12; DB 3; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||  
DB 16 CCCAGTTGAAGT 5

## RESULT 28

US-09-371-772B-1646/c  
; Sequence 1646, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1646  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-1646

Query Match 60.0%; Score 12; DB 3; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||  
DB 17 CCCAGTTGAAGT 6

## RESULT 29

US-09-371-772B-1647/c  
; Sequence 1647, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1647  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-1647

Query Match 60.0%; Score 12; DB 3; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||  
DB 16 CCCAGTTGAAGT 5

## RESULT 30

US-09-371-772B-6253/c  
; Sequence 6253, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6253  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-6253

Query Match 60.0%; Score 12; DB 3; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||  
DB 15 CCCAGTTGAAGT 4

## RESULT 31

US-09-371-772B-6254/c  
; Sequence 6254, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00,876-J (237/198)



; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6254  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-6254

Query Match 60.0%; Score 12; DB 3; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14  
| | | | | | | | | | | | | | | | | |  
Db 12 CCCAGTTGAAGT 1

RESULT 32  
US-09-685-664B-1646/c  
; Sequence 1646, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1646  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-685-664B-1646

Query Match 60.0%; Score 12; DB 3; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14  
| | | | | | | | | | | | | | | | | |  
Db 17 CCCAGTTGAAGT 6

RESULT 33  
US-09-685-664B-1647/c  
; Sequence 1647, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1647  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-685-664B-1647

Query Match 60.0%; Score 12; DB 3; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14  
| | | | | | | | | | | | | | | | | |  
Db 16 CCCAGTTGAAGT 5

RESULT 34  
US-10-138-674B-1646/c  
; Sequence 1646, Application US/10138674B  
; Patent No. 7034009  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674B  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1646  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674B-1646

Query Match 60.0%; Score 12; DB 5; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14  
| | | | | | | | | | | | | | | | | |  
Db 17 CCCAGTTGAAGT 6

RESULT 35  
US-10-138-674B-1647/c  
; Sequence 1647, Application US/10138674B  
; Patent No. 7034009  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

```
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1647
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-1647

Query Match      60.0%; Score 12; DB 5; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
   |||||
Db 16 CCCAGTTGAAGT 5

RESULT 36
US-10-138-674B-6253/c
; Sequence 6253, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6253
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-6253

Query Match      60.0%; Score 12; DB 5; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
   |||||
Db 15 CCCAGTTGAAGT 4

RESULT 37
US-10-138-674B-6254/c
; Sequence 6254, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6254
```

```
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-6254

Query Match      60.0%; Score 12; DB 5; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
   |||||
Db 12 CCCAGTTGAAGT 1

RESULT 38
US-10-138-674B-8571/c
; Sequence 8571, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8571
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-8571

Query Match      60.0%; Score 12; DB 5; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
   |||||
Db 14 CCCAGTTGAAGT 3

RESULT 39
US-10-310-914B-1191074/c
; Sequence 1191074, Application US/10310914B
; Patent No. 7250496
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914B
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388411
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1191074
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914B-1191074

Query Match      67.0%; Score 13.4; DB 6; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 5.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 4 CCAAGTTGAAGTTGCC 18  
|||||  
Db 17 CCAAGTTGAAGTTCCC 3

## RESULT 40

US-08-401-512-16  
; Sequence 16, Application US/08401512  
; Patent No. 5599673  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Curran, Mark E.  
; APPLICANT: Wang, Qing  
; TITLE OF INVENTION: Long QT Syndrome Genes  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3917  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/401,512  
; FILING DATE: 09-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Stephen A.  
; REGISTRATION NUMBER: 38,609  
; REFERENCE/DOCKET NUMBER: 19780-113879  
; TELEPHONE: 202-962-4848  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-401-512-16

Query Match 42.0%; Score 8.4; DB 2; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 1.5e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCCAGTTGA 11  
|||||  
Db 1 CCCCAGTTGA 10

## RESULT 41

US-08-738-381-48/c  
; Sequence 48, Application US/08738381  
; Patent No. 6083694  
; GENERAL INFORMATION:  
; APPLICANT: John A. Hardy, Alison M. Goate  
; TITLE OF INVENTION: Method for Elucidation and  
; TITLE OF INVENTION: Detection of Polymorphisms, Splice Variants and  
; TITLE OF INVENTION: Proximal Coding Using Intronic Sequences of the  
; TITLE OF INVENTION: Mutations Alzheimer's S182 Gene  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road, P.O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb  
; MEDIUM TYPE: STORAGE  
; COMPUTER: IBM 486  
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/738,381  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/007,048  
; FILING DATE: October 25, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: P50388  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5024  
; TELEFAX: 610-270-5090  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: NO  
US-08-738-381-48

Query Match 42.0%; Score 8.4; DB 3; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 1.5e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16  
|||||  
Db 10 GTTGATGTTG 1

## RESULT 42

US-10-078-958-50/c  
; Sequence 50, Application US/10078958  
; Patent No. 7064244  
; GENERAL INFORMATION:  
; APPLICANT: JAKOBOVITS, AYA  
; APPLICANT: KUCHERLAPATI, RAJU  
; APPLICANT: KLAPHOLZ, SUSAN  
; APPLICANT: MENDEZ, MICHAEL J.  
; APPLICANT: GREEN, LARRY  
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING  
; TITLE OF INVENTION: PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED  
; FILE REFERENCE: CELL 4.18 CON  
; CURRENT APPLICATION NUMBER: US/10/078,958  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 08/759,620  
; PRIOR FILING DATE: 1996-12-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-078-958-50

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 1.5e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTG 10  
| | | | | | | |  
Db 12 GCCCCAGTAG 3

## RESULT 43

US-10-078-958-59/c  
; Sequence 59, Application US/10078958  
; Patent No. 7064244  
; GENERAL INFORMATION:  
; APPLICANT: JAKOBOVITS, AYA  
; APPLICANT: KUCHERLAPATI, RAJU  
; APPLICANT: KLAPHOLZ, SUSAN  
; APPLICANT: MENDEZ, MICHAEL J.  
; APPLICANT: GREEN, LARRY  
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING  
; TITLE OF INVENTION: PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED  
; TITLE OF INVENTION: THEREFROM  
; FILE REFERENCE: CELL 4.18 CON  
; CURRENT APPLICATION NUMBER: US/10/078,958  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 08/759,620  
; PRIOR FILING DATE: 1996-12-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 59  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-078-958-59

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 1.5e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTG 10  
| | | | | | | |  
Db 12 GCCCCAGTAG 3

Search completed: December 3, 2007, 17:46:21  
Job time : 223 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:28:31 ; Search time 6392 Seconds  
(without alignments)  
74.253 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagttgaagttgccgt 20

Scoring table: Oligo\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 31364175 seqs, 1186555624 residues

Word size : 1

Total number of hits satisfying chosen parameters: 37000596

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA Main:

1: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
6: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09D\_PUBCOMB.seq.\*  
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8: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
9: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
10: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
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12: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
13: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
14: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
15: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
16: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10J\_PUBCOMB.seq.\*  
17: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10K\_PUBCOMB.seq.\*  
18: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
19: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11B\_PUBCOMB.seq.\*  
20: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11C\_PUBCOMB.seq.\*  
21: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11D\_PUBCOMB.seq.\*  
22: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11E\_PUBCOMB.seq.\*  
23: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11F\_PUBCOMB.seq.\*  
24: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11G\_PUBCOMB.seq.\*  
25: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11H\_PUBCOMB.seq.\*  
26: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11I\_PUBCOMB.seq.\*  
27: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11J\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-908-147-64
2	20	100.0	20	9	US-10-728-509-64
3	18	90.0	20	3	US-09-908-147-65
4	18	90.0	20	9	US-10-728-509-65
5	16	80.0	20	3	US-09-908-147-119
6	16	80.0	20	9	US-10-728-509-119

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTTGCCGT 20  
DB 1 GCCCCAGTTGAAGTTGCCGT 20

7 15 75.0 18 3 US-09-908-147-5  
8 15 75.0 18 9 US-10-728-509-5  
9 15 75.0 25 12 US-10-932-182A-95621  
10 15 75.0 25 12 US-11-217-929-95621  
c 11 14 70.0 19 15 US-10-714-333A-764639  
c 12 14 70.0 19 15 US-11-083-784-764639  
c 13 14 70.0 19 20 US-11-101-244-764639  
c 14 14 70.0 25 9 US-10-719-956-88092  
c 15 14 70.0 25 9 US-10-719-956-179809  
c 16 14 70.0 25 18 US-11-036-317-560158  
c 17 14 70.0 25 20 US-11-121-849-128966  
c 18 14 70.0 25 20 US-11-121-849-128967  
c 19 14 70.0 25 23 US-11-371-354-19250  
c 20 14 70.0 33 24 US-11-406-808B-596981  
c 21 14 70.0 37 8 US-10-331-907-146  
c 22 13 65.0 19 15 US-10-714-333A-726378  
c 23 13 65.0 19 15 US-10-714-333A-726385  
c 24 13 65.0 19 15 US-10-714-333A-805351  
c 25 13 65.0 19 15 US-10-714-333A-805410  
c 26 13 65.0 19 15 US-10-714-333A-1208394  
c 27 13 65.0 19 15 US-10-714-333A-1208423  
c 28 13 65.0 19 15 US-10-714-333A-1546246  
c 29 13 65.0 19 19 US-11-083-784-726378  
c 30 13 65.0 19 19 US-11-083-784-726385  
c 31 13 65.0 19 19 US-11-083-784-805351  
c 32 13 65.0 19 19 US-11-083-784-805410  
c 33 13 65.0 19 19 US-11-083-784-1208394  
c 34 13 65.0 19 19 US-11-083-784-1208423  
c 35 13 65.0 19 19 US-11-083-784-1546246  
c 36 13 65.0 19 20 US-11-101-244-726378  
c 37 13 65.0 19 20 US-11-101-244-726385  
c 38 13 65.0 19 20 US-11-101-244-805351  
c 39 13 65.0 19 20 US-11-101-244-805410  
c 40 13 65.0 19 20 US-11-101-244-1208394  
c 41 13 65.0 19 20 US-11-101-244-1208423  
c 42 13 65.0 19 20 US-11-101-244-1546246  
c 43 13 65.0 20 3 US-09-908-147-118  
c 44 13 65.0 20 3 US-09-908-147-120  
c 45 13 65.0 20 8 US-10-032-585-5524

#### ALIGNMENTS

RESULT 1  
US-09-908-147-64  
; Sequence 64, Application US/09908147  
; Publication No. US2003014221A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/09/908,147  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 64  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-908-147-64

```
RESULT 2
US-10-728-509-64
; Sequence 64, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-64

Query Match      90.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCCCCAGTTGAAGTGCCT 20
        |||||
Db       1  GCCCCAGTTGAAGTGCCT 20

RESULT 3
US-09-908-147-65
; Sequence 65, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-65

Query Match      90.0%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCCCCAGTTGAAGTTGCC 18
        |||||
Db       3  GCCCCAGTTGAAGTTGCC 20

RESULT 4
US-10-728-509-65
; Sequence 65, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-65

Query Match      90.0%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCCCCAGTTGAAGTTGCC 18
        |||||
Db       3  GCCCCAGTTGAAGTTGCC 20

RESULT 5
US-09-908-147-119
; Sequence 119, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-119

Query Match      80.0%; Score 16; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  CCCAGTTGAAGTTGCC 18
        |||||
Db       1  CCCAGTTGAAGTTGCC 16

RESULT 6
US-10-728-509-119
; Sequence 119, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-119

Query Match      80.0%; Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-65

Query Match      90.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCCCCAGTTGAAGTTGCC 18
        |||||
Db       3  GCCCCAGTTGAAGTTGCC 20

RESULT 5
US-09-908-147-119
; Sequence 119, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-119

Query Match      80.0%; Score 16; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  CCCAGTTGAAGTTGCC 18
        |||||
Db       1  CCCAGTTGAAGTTGCC 16

RESULT 6
US-10-728-509-119
; Sequence 119, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-119

Query Match      80.0%; Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 3 CCCAGTTGAAGTTGCC 18  
Db 1 CCCAGTTGAAGTTGCC 16

## RESULT 7

US-09-908-147-5  
; Sequence 5, Application US/09908147  
; Publication No. US20030144221A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/09/908,147  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-09-908-147-5

Query Match 75.0%; Score 15; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTT 15  
Db 4 GCCCCAGTTGAAGTT 18

## RESULT 8

US-10-728-509-5  
; Sequence 5, Application US/10728509  
; Publication No. US20040077583A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-10-728-509-5

Query Match 75.0%; Score 15; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTT 15  
Db 4 GCCCCAGTTGAAGTT 18

## RESULT 9

US-10-932-182A-95621  
; Sequence 95621, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 95621  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-95621

Query Match 75.0%; Score 15; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGTTGC 17  
Db 10 CCCAGTTGAAGTTGC 24

## RESULT 10

US-11-217-529-95621  
; Sequence 95621, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 95621  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-95621

Query Match 75.0%; Score 15; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGTTGC 17  
Db 10 CCCAGTTGAAGTTGC 24

## RESULT 11

US-10-714-333A-764639/c  
; Sequence 764639, Application US/10714333A  
; Publication No. US20070031844A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333A  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050

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; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-764639

Query Match          70.0%; Score 14; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 12
US-11-083-784-764639/c
; Sequence 764639, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-764639

Query Match          70.0%; Score 14; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 13
US-11-101-244-764639/c
; Sequence 764639, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-764639

Query Match          70.0%; Score 14; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCGT 20
Db 16 GTTGAAGTTGCCGT 3

RESULT 14
US-10-719-956-88092
; Sequence 88092, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-88092

Query Match          70.0%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGC 17
Db 9 CCAGTTGAAGTTGC 22

RESULT 15
US-10-719-956-179809/c
; Sequence 179809, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 179809
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-179809

Query Match          70.0%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 7 GTTGAAGTTGCCGT 20  
| | | | | | | | | |  
Db 21 GTTGAAGTTGCCGT 8

Search completed: December 3, 2007, 18:15:06  
Job time : 6395 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:33:10 ; Search time 754 Seconds  
(without alignments)  
25.967 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccacgttgagttgccgt 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2833015 seqs, 489481754 residues

Word size : 1

Total number of hits satisfying chosen parameters: 4885892

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : 1: /EMC\_Celerra\_SIDS2/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*

- 2: /EMC\_Celerra\_SIDS2/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /EMC\_Celerra\_SIDS2/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /EMC\_Celerra\_SIDS2/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
5: /EMC\_Celerra\_SIDS2/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
6: /EMC\_Celerra\_SIDS2/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /EMC\_Celerra\_SIDS2/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
8: /EMC\_Celerra\_SIDS2/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
9: /EMC\_Celerra\_SIDS2/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
C 1	14	70.0	19	US-11-095-383-764639 Sequence 764639
C 2	14	70.0	25	US-11-095-599-593353 Sequence 593353
C 3	13	65.0	19	US-11-095-383-726378 Sequence 726378
C 4	13	65.0	19	US-11-095-383-726385 Sequence 726385
C 5	13	65.0	19	US-11-095-383-805351 Sequence 805351
C 6	13	65.0	19	US-11-095-383-805410 Sequence 805410
C 7	13	65.0	19	US-11-095-383-1208394 Sequence 1208394
C 8	13	65.0	19	US-11-095-383-1208423 Sequence 1208423
C 9	13	65.0	19	US-11-095-383-1546246 Sequence 1546246
C 10	13	65.0	25	US-11-095-599-241845 Sequence 241845
C 11	13	65.0	25	US-11-095-599-268739 Sequence 268739
C 12	13	65.0	25	US-11-095-599-607730 Sequence 607730
C 13	12	60.0	19	US-11-095-383-4103 Sequence 4103
C 14	12	60.0	19	US-11-095-383-726390 Sequence 726390
C 15	12	60.0	19	US-11-095-383-1132462 Sequence 1132462
C 16	12	60.0	19	US-11-095-383-1132508 Sequence 1132508
C 17	12	60.0	19	US-11-095-383-1208461 Sequence 1208461
C 18	12	60.0	19	US-11-095-383-1250562 Sequence 1250562
C 19	12	60.0	25	US-11-095-599-68029 Sequence 68029
C 20	12	60.0	25	US-11-095-599-127413 Sequence 127413
C 21	12	60.0	25	US-11-095-599-177427 Sequence 177427
C 22	12	60.0	25	US-11-095-599-288862 Sequence 288862
C 23	12	60.0	25	US-11-095-599-352349 Sequence 352349
C 24	12	60.0	25	US-11-095-599-357863 Sequence 357863

C 25	12	60.0	25	7	US-11-095-599-487464	Sequence 487464,
C 26	12	60.0	29	7	US-11-095-603-928	Sequence 928, App
C 27	12	60.0	29	7	US-11-095-603-928	Sequence 928, App
C 28	12	60.0	29	7	US-11-095-579-928	Sequence 928, App
C 29	12	60.0	29	7	US-11-095-610-928	Sequence 928, App
C 30	12	60.0	29	7	US-11-095-598-928	Sequence 928, App
C 31	11	55.0	19	6	US-10-553-729-821	Sequence 821, App
C 32	11	55.0	19	6	US-10-553-729-2472	Sequence 2472, App
C 33	11	55.0	19	8	US-11-095-383-4169	Sequence 4169, App
C 34	11	55.0	19	8	US-11-095-383-64620	Sequence 64620, A
C 35	11	55.0	19	8	US-11-095-383-104611	Sequence 104611,
C 36	11	55.0	19	8	US-11-095-383-104627	Sequence 104627,
C 37	11	55.0	19	8	US-11-095-383-189244	Sequence 189244,
C 38	11	55.0	19	8	US-11-095-383-189290	Sequence 189290,
C 39	11	55.0	19	8	US-11-095-383-208863	Sequence 208863,
C 40	11	55.0	19	8	US-11-095-383-236981	Sequence 236981,
C 41	11	55.0	19	8	US-11-095-383-258320	Sequence 258320,
C 42	11	55.0	19	8	US-11-095-383-258408	Sequence 258408,
C 43	11	55.0	19	8	US-11-095-383-265304	Sequence 265304,
C 44	11	55.0	19	8	US-11-095-383-265334	Sequence 265334,
C 45	11	55.0	19	8	US-11-095-383-265443	Sequence 265443,

ALIGNMENTS

RESULT 1  
US-11-095-383-764639/c  
; Sequence 764639, Application US/11095383  
; Publication No. US20070207974A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scarsdale, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/095,383  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 159191  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-095-383-764639

Query Match 70.0%; Score 14; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20  
Db 16 GTTGAAGTTGCCGT 3

RESULT 2  
US-11-095-599-593353/c  
; Sequence 593353, Application US/11695599  
; Publication No. US20070243546A1  
; GENERAL INFORMATION:  
; APPLICANT: Yan Cao  
; APPLICANT: Shivani Nautiyal  
; APPLICANT: Garry Miyada  
; APPLICANT: Chris Davies

```
; APPLICANT: Gangwu Mei
; APPLICANT: Alan Williams
; APPLICANT: Eric Schell
; APPLICANT: John E. Blume
; TITLE OF INVENTION: Analysis of Methylation Using Nucleic Acid Arrays
; FILE REFERENCE: 3791.1
; CURRENT APPLICATION NUMBER: US/11/695,599
; CURRENT FILING DATE: 2007-04-02
; PRIOR APPLICATION NUMBER: 60/788,520
; PRIOR FILING DATE: 2006-03-31
; NUMBER OF SEQ ID NOS: 743256
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 593353
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-695-599-593353

Query Match      70.0%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CCAGTTGAAGTTGCC 17
DB      15 CCAGTTGAAGTTGC 2

RESULT 3
US-11-095-383-726378/c
; Sequence 726378, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726378
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-726378

Query Match      65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
DB      17 AGTTGAAGTTGCC 5

RESULT 4
US-11-095-383-726385/c
; Sequence 726385, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726385
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-726385

Query Match      65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGCC 18
DB      18 AGTTGAAGTTGCC 6

RESULT 5
US-11-095-383-805351/c
; Sequence 805351, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/095,383
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 805351
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-095-383-805351

Query Match      65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TTGAAGTTGCCGT 20
DB      15 TTGAAGTTGCCGT 3

RESULT 6
US-11-095-383-805410/c
; Sequence 805410, Application US/11095383
; Publication No. US20070207974A1
; GENERAL INFORMATION:
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; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/095,383  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR FILING DATE: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 805410  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-095-383-805410

Query Match 65.0%; Score 13; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20  
Db 14 TTGAAGTTGCCGT 2

## RESULT 7

US-11-095-383-1208394/c  
; Sequence 1208394, Application US/11095383  
; Publication No. US20070207974A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/095,383  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR FILING DATE: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1208394  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-095-383-1208394

Query Match 65.0%; Score 13; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTG 16  
Db 16 CCAGTTGAAGTTG 4

## RESULT 8

US-11-095-383-1208423/c

; Sequence 1208423, Application US/11095383  
; Publication No. US20070207974A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/095,383  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR FILING DATE: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1208423  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-095-383-1208423

Query Match 65.0%; Score 13; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTG 16  
Db 17 CCAGTTGAAGTTG 5

## RESULT 9

US-11-095-383-1546246/c  
; Sequence 1546246, Application US/11095383  
; Publication No. US20070207974A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/095,383  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR FILING DATE: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1546246  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-095-383-1546246

Query Match 65.0%; Score 13; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19  
Db 19 GTTGAAGTTGCCG 7

## RESULT 10

US-11-695-599-241845/c  
; Sequence 241845, Application US/11695599  
; Publication No. US20070243546A1  
; GENERAL INFORMATION:  
; APPLICANT: Yan Cao  
; APPLICANT: Shivani Nautiyal  
; APPLICANT: Garry Miyada  
; APPLICANT: Chris Davies  
; APPLICANT: Gangwu Mei  
; APPLICANT: Alan Williams  
; APPLICANT: Eric Schell  
; APPLICANT: John E. Blume  
; TITLE OF INVENTION: Analysis of Methylation Using Nucleic Acid Arrays  
; FILE REFERENCE: 3791.1  
; CURRENT APPLICATION NUMBER: US/11/695,599  
; CURRENT FILING DATE: 2007-04-02  
; PRIOR APPLICATION NUMBER: 60/788,520  
; PRIOR FILING DATE: 2006-03-31  
; NUMBER OF SEQ ID NOS: 743256  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 241845  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-695-599-241845

Query Match 65.0%; Score 13; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTCGCGT 20  
| | | | | | | | | |  
DB 16 TTGAAGTTCGCGT 4

## RESULT 11

US-11-695-599-268739/c  
; Sequence 268739, Application US/11695599  
; Publication No. US20070243546A1  
; GENERAL INFORMATION:  
; APPLICANT: Yan Cao  
; APPLICANT: Shivani Nautiyal  
; APPLICANT: Garry Miyada  
; APPLICANT: Chris Davies  
; APPLICANT: Gangwu Mei  
; APPLICANT: Alan Williams  
; APPLICANT: Eric Schell  
; APPLICANT: John E. Blume  
; TITLE OF INVENTION: Analysis of Methylation Using Nucleic Acid Arrays  
; FILE REFERENCE: 3791.1  
; CURRENT APPLICATION NUMBER: US/11/695,599  
; CURRENT FILING DATE: 2007-04-02  
; PRIOR APPLICATION NUMBER: 60/788,520  
; PRIOR FILING DATE: 2006-03-31  
; NUMBER OF SEQ ID NOS: 743256  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 268739  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-695-599-268739

Query Match 65.0%; Score 13; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13  
| | | | | | | | | |  
DB 19 GCCCCAGTTGAAG 7

## RESULT 12

US-11-695-599-607730/c  
; Sequence 607730, Application US/11695599  
; Publication No. US20070243546A1  
; GENERAL INFORMATION:  
; APPLICANT: Yan Cao  
; APPLICANT: Shivani Nautiyal  
; APPLICANT: Garry Miyada  
; APPLICANT: Chris Davies  
; APPLICANT: Gangwu Mei  
; APPLICANT: Alan Williams  
; APPLICANT: Eric Schell  
; APPLICANT: John E. Blume  
; TITLE OF INVENTION: Analysis of Methylation Using Nucleic Acid Arrays  
; FILE REFERENCE: 3791.1  
; CURRENT APPLICATION NUMBER: US/11/695,599  
; CURRENT FILING DATE: 2007-04-02  
; PRIOR APPLICATION NUMBER: 60/788,520  
; PRIOR FILING DATE: 2006-03-31  
; NUMBER OF SEQ ID NOS: 743256  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 607730  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-695-599-607730

Query Match 65.0%; Score 13; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTT 15  
| | | | | | | | | |  
DB 25 CCCAGTTGAAGTT 13

## RESULT 13

US-11-095-383-4103/c  
; Sequence 4103, Application US/11095383  
; Publication No. US20070207974A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scarsinge, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/095,383  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 4103  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-095-383-4103

Query Match 60.0%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16  
| | | | | | | | | |  
DB 12 CAGTTGAAGTTG 1

## RESULT 14

US-11-095-383-726390/c  
; Sequence 726390, Application US/11095383  
; Publication No. US20070207974A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/095,383  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 726390  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-095-383-726390

Query Match 60.0%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred.No. 6.7e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18  
Db 19 GTTGAAGTTGCC 8

## RESULT 15

US-11-095-383-1132462/c  
; Sequence 1132462, Application US/11095383  
; Publication No. US20070207974A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/095,383  
; CURRENT FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1132462  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-095-383-1132462

Query Match 60.0%; Score 12; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred.No. 6.7e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCC 19

Db 18 TTGAAGTTGCC 7

Search completed: December 3, 2007, 16:58:28  
Job time : 755 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:22:33 ; Search time 206 Seconds  
(without alignments)  
72.858 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagttgaagttgccgt 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 614577 seqs, 375217992 residues

Word size: 1

Total number of hits satisfying chosen parameters: 433342

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database: Pending Patents NA New:\*

- 1: /EMC\_Celerra\_SIDS2/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US06\_NEW\_COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US07\_NEW\_COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US08\_NEW\_COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US09\_NEW\_COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US10\_NEW\_COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US11\_NEW\_COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	16	80.0	22	1	PCT-US07-11121-41
c 2	12	60.0	32	7	US-11-884-818-26
c 3	12	60.0	32	7	US-11-884-818-29
c 4	12	60.0	35	7	US-11-909-031-55
c 5	11	55.0	19	7	US-11-977-128-13195
c 6	11	55.0	19	7	US-11-977-128-21540
c 7	11	55.0	20	8	US-60-986-286-208
c 8	11	55.0	21	6	US-10-923-3798B-1922
c 9	11	55.0	21	6	US-10-923-3798B-1923
c 10	11	55.0	21	6	US-10-923-3798B-1950
c 11	11	55.0	21	6	US-10-923-3798B-1951
c 12	11	55.0	21	6	US-10-923-3798B-1978
c 13	11	55.0	21	6	US-10-923-3798B-1979
c 14	11	55.0	21	6	US-10-923-3798B-2006
c 15	11	55.0	21	6	US-10-923-3798B-2007
c 16	11	55.0	21	6	US-10-923-3798B-2034
c 17	11	55.0	21	6	US-10-923-3798B-2035
c 18	11	55.0	21	6	US-10-923-3798B-2062
c 19	11	55.0	21	6	US-10-923-3798B-2063
c 20	11	55.0	21	6	US-10-923-3798B-2090
c 21	11	55.0	21	6	US-10-923-3798B-2091
c 22	11	55.0	21	6	US-10-923-3798B-2118
c 23	11	55.0	21	6	US-10-923-3798B-2119
c 24	11	55.0	21	6	US-10-923-3798B-2146
c 25	11	55.0	21	6	US-10-923-3798B-2147

26	11	55.0	21	6	US-10-923-3798B-2174	Sequence 2174, Ap
27	11	55.0	21	6	US-10-923-3798B-2175	Sequence 2175, Ap
28	11	55.0	21	6	US-10-923-3798B-2202	Sequence 2202, Ap
29	11	55.0	21	6	US-10-923-3798B-2203	Sequence 2203, Ap
30	11	55.0	21	6	US-10-923-3798B-2230	Sequence 2230, Ap
31	11	55.0	21	6	US-10-923-3798B-2231	Sequence 2231, Ap
32	11	55.0	21	7	US-11-746-864-532	Sequence 532, App
33	11	55.0	21	7	US-11-746-864-534	Sequence 534, App
c 34	11	55.0	23	6	US-10-923-3798B-1508	Sequence 1508, Ap
c 35	11	55.0	23	6	US-10-923-3798B-1509	Sequence 1509, Ap
c 36	11	55.0	29	7	US-11-737-025-34	Sequence 34, Appl
c 37	11	55.0	33	7	US-11-836-770-11	Sequence 11, Appl
c 38	11	55.0	40	6	US-10-548-533-5	Sequence 5, Appli
c 39	10	50.0	19	7	US-11-001-347B-692	Sequence 692, App
c 40	10	50.0	19	7	US-11-001-347B-763	Sequence 763, App
c 41	10	50.0	19	7	US-11-977-128-660	Sequence 660, App
c 42	10	50.0	19	7	US-11-977-128-16883	Sequence 16883, A
c 43	10	50.0	19	8	US-60-956-679-75	Sequence 75, Appl
c 44	10	50.0	19	8	US-60-934-954-153	Sequence 153, App
c 45	10	50.0	20	6	US-10-576-900-175	Sequence 175, App

ALIGNMENTS

RESULT 1  
PCT-US07-11121-41/c  
; Sequence 41, Application PC/TUS0711121  
; GENERAL INFORMATION:  
; APPLICANT: Hitachi Chemical Co., Ltd.  
; APPLICANT: Hitachi Chemical Research Center, Inc.  
; APPLICANT: Mitsuhashi, Masato  
; APPLICANT: Ibara, Kazuhiko  
; TITLE OF INVENTION: Method for Testing Drug Sensitivity in  
; TITLE OF INVENTION: Solid Tumors by Quantifying mRNA Expression in Thinly-Sliced  
; TITLE OF INVENTION: Tumor Tissue  
; FILE REFERENCE: HITACHI.081VPC  
; CURRENT APPLICATION NUMBER: PCT/US07/11121  
; CURRENT FILING DATE: 2007-09-19  
; PRIOR APPLICATION NUMBER: PCT/US2007/011121  
; PRIOR FILING DATE: 2007-05-08  
; PRIOR APPLICATION NUMBER: US 60/798,674  
; PRIOR FILING DATE: 2006-05-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: BAX forward primer sequence  
PCT-US07-11121-41

Query Match 80.0%; Score 16; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20  
|||||  
DB 22 CAGTTGAAGTTGCCGT 7

RESULT 2  
US-11-884-818-26  
; Sequence 26, Application US/11884818  
; GENERAL INFORMATION:  
; APPLICANT: Duwenig, Elke  
; APPLICANT: Loyall, Linda P  
; TITLE OF INVENTION: EXPRESSION CASSETTES FOR SEED-PREFERENTIAL EXPRESSION IN PLANTS  
; FILE REFERENCE: 13987-00085-US  
; CURRENT APPLICATION NUMBER: US/11/884,818  
; CURRENT FILING DATE: 2007-09-06  
; PRIOR APPLICATION NUMBER: PCT/EP2006/060266

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; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 05004248.0
; PRIOR FILING DATE: 2005-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.4
; SEQ ID NO 26
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-11-884-818-26

Query Match          60.0%; Score 12; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 16 AGTTGAAGTTGC 27

RESULT 3
US-11-884-818-29
; Sequence 29, Application US/11884818
; GENERAL INFORMATION:
; APPLICANT: Duwainig, Elke
; APPLICANT: Loyall, Linda P
; TITLE OF INVENTION: EXPRESSION CASSETTES FOR SEED-PREFERENTIAL EXPRESSION IN PLANTS
; FILE REFERENCE: 13987-00065-US
; CURRENT APPLICATION NUMBER: US/11/884,818
; CURRENT FILING DATE: 2007-09-06
; PRIOR APPLICATION NUMBER: PCT/EP2006/060266
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 05004248.0
; PRIOR FILING DATE: 2005-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.4
; SEQ ID NO 29
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-11-884-818-29

Query Match          60.0%; Score 12; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 16 AGTTGAAGTTGC 27

RESULT 4
US-11-909-031-55
; Sequence 55, Application US/11909031
; GENERAL INFORMATION:
; APPLICANT: Astellas Pharma Inc.
; APPLICANT: Endoh, Hideki
; APPLICANT: YOKOTA, Hiroyuki
; APPLICANT: HAYAKAWA, Masahiko
; APPLICANT: SOGA, Shinji
; TITLE OF INVENTION: A method for identification of drug targets and a method of
; screening antidiabetic drug using the identified target
; FILE REFERENCE: Q103930
; CURRENT APPLICATION NUMBER: US/11/909,031
; CURRENT FILING DATE: 2007-09-18
; PRIOR APPLICATION NUMBER: JP2005-234673
; PRIOR FILING DATE: 2005-08-12
; PRIOR APPLICATION NUMBER: JP2005-279582
; PRIOR FILING DATE: 2005-09-27
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; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer sequence
US-11-909-031-55

Query Match          60.0%; Score 12; DB 7; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16
Db 10 CAGTTGAAGTTG 21

RESULT 5
US-11-977-128-13195
; Sequence 13195, Application US/11977128
; GENERAL INFORMATION:
; APPLICANT: KHVOROVA, Anastasia
; APPLICANT: REYNOLDS, Angela
; APPLICANT: LEAKE, Devin
; APPLICANT: MARSHALL, William
; APPLICANT: READ, Steven
; APPLICANT: SCARINGE, Stephen
; TITLE OF INVENTION: siRNA Targeting Kinases
; FILE REFERENCE: DHARMA 2100-US74
; CURRENT APPLICATION NUMBER: US/11/977,128
; CURRENT FILING DATE: 2007-10-31
; PRIOR APPLICATION NUMBER: 10/940,892
; PRIOR FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: PCT/US04/14885
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,136
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 22603
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 13195
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-977-128-13195

Query Match          55.0%; Score 11; DB 7; Length 19;
Best Local Similarity 63.6%; Pred. No. 1.3e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 7 AGUGAAGUUG 17

RESULT 6
US-11-977-128-21540
; Sequence 21540, Application US/11977128
; GENERAL INFORMATION:
; APPLICANT: KHVOROVA, Anastasia
; APPLICANT: REYNOLDS, Angela
; APPLICANT: LEAKE, Devin
; APPLICANT: MARSHALL, William
; APPLICANT: READ, Steven
; APPLICANT: SCARINGE, Stephen
; TITLE OF INVENTION: siRNA Targeting Kinases
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; FILE REFERENCE: DHARMA 2100-US74  
; CURRENT APPLICATION NUMBER: US/11/977,128  
; CURRENT FILING DATE: 2007-10-31  
; PRIOR APPLICATION NUMBER: 10/940,892  
; PRIOR FILING DATE: 2004-09-14  
; PRIOR APPLICATION NUMBER: PCT/US04/14885  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/426,136  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; NUMBER OF SEQ ID NOS: 22603  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21540  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-11-977-128-21540

Query Match 55.0%; Score 11; DB 7; Length 19;  
Best Local Similarity 63.6%; Pred. No. 1.3e+03;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16  
||:|||||:  
Db 2 AGUUGAAGUUG 12

RESULT 7  
US-60-986-286-208/c  
; Sequence 208, Application US/60986286  
; GENERAL INFORMATION:  
; APPLICANT: Susan M. Freier  
; APPLICANT: Rosanne M. Crooke  
; APPLICANT: Mark J. Graham  
; APPLICANT: Kristina Lemonidis Tarbet  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Diane Tribble  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: METHODS FOR TREATING  
; TITLE OF INVENTION: HYPERCHOLESTEROLEMIA  
; FILE REFERENCE: BIOL0090US.L3  
; CURRENT APPLICATION NUMBER: US/60/986,286  
; CURRENT FILING DATE: 2007-11-07  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 208  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-60-986-286-208

Query Match 55.0%; Score 11; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCC 18  
|||||  
Db 11 TTGAAGTTGCC 1

RESULT 8  
US-10-923-379B-1922/c  
; Sequence 1922, Application US/10923379B  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James

; APPLICANT: Beigelman, Leonid  
; APPLICANT: Usman, Nassim  
; APPLICANT: Haeblerli, Peter  
; APPLICANT: Chowrira, Bharat  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene  
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway  
; FILE REFERENCE: 03-040-D; (400.233)  
; CURRENT APPLICATION NUMBER: US/10/923,379B  
; CURRENT FILING DATE: 2004-08-20  
; NUMBER OF SEQ ID NOS: 2360  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1922  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(19)  
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this  
; OTHER INFORMATION: sequence  
US-10-923-379B-1922

Query Match 55.0%; Score 11; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGC 17  
|||||  
Db 18 GTTGAAGTTGC 8

RESULT 9  
US-10-923-379B-1923/c  
; Sequence 1923, Application US/10923379B  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Usman, Nassim  
; APPLICANT: Haeblerli, Peter  
; APPLICANT: Chowrira, Bharat  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene  
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway  
; FILE REFERENCE: 03-040-D; (400.233)  
; CURRENT APPLICATION NUMBER: US/10/923,379B  
; CURRENT FILING DATE: 2004-08-20  
; NUMBER OF SEQ ID NOS: 2360  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1923  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(19)  
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this  
; OTHER INFORMATION: sequence  
US-10-923-379B-1923

Query Match 55.0%; Score 11; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGC 17  
|||||  
Db 17 GTTGAAGTTGC 7

RESULT 10  
US-10-923-379B-1950  
; Sequence 1950, Application US/10923379B  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Usman, Nassim  
; APPLICANT: Haerberli, Peter  
; APPLICANT: Chowrira, Bharat  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene  
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway  
; FILE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 03-040-D; (400.233)  
; CURRENT APPLICATION NUMBER: US/10/923,379B  
; CURRENT FILING DATE: 2004-08-20  
; NUMBER OF SEQ ID NOS: 2360  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1950  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; NAME/KEY: misc feature  
; LOCATION: (1)..(19)  
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this  
; OTHER INFORMATION: sequence  
US-10-923-379B-1950

Query Match 55.0%; Score 11; DB 6; Length 21;  
Best Local Similarity 63.6%; Pred. No. 1.3e+03;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGC 17  
|:|||||:  
Db 2 GUUGAAGUUGC 12

RESULT 11  
US-10-923-379B-1951  
; Sequence 1951, Application US/10923379B  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Usman, Nassim  
; APPLICANT: Haerberli, Peter  
; APPLICANT: Chowrira, Bharat  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene  
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway  
; FILE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 03-040-D; (400.233)  
; CURRENT APPLICATION NUMBER: US/10/923,379B  
; CURRENT FILING DATE: 2004-08-20  
; NUMBER OF SEQ ID NOS: 2360  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1951  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; NAME/KEY: misc feature  
; LOCATION: (1)..(19)  
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this  
; OTHER INFORMATION: sequence  
US-10-923-379B-1951

Query Match 55.0%; Score 11; DB 6; Length 21;

Best Local Similarity 63.6%; Pred. No. 1.3e+03;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGC 17  
|:|||||:  
Db 3 GUUGAAGUUGC 13

RESULT 12  
US-10-923-379B-1978/c  
; Sequence 1978, Application US/10923379B  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Usman, Nassim  
; APPLICANT: Haerberli, Peter  
; APPLICANT: Chowrira, Bharat  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene  
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway  
; FILE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 03-040-D; (400.233)  
; CURRENT APPLICATION NUMBER: US/10/923,379B  
; CURRENT FILING DATE: 2004-08-20  
; NUMBER OF SEQ ID NOS: 2360  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1978  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: 5'-3 attached terminal deoxybasic moiety  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (3)..(6)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (12)..(15)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (18)..(19)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(19)  
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this  
; OTHER INFORMATION: sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (21)..(21)  
; OTHER INFORMATION: 3'-3 attached terminal deoxybasic moiety  
US-10-923-379B-1978

Query Match 55.0%; Score 11; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGC 17  
|:|||||:  
Db 18 GTTGAAGTTGC 8

RESULT 13

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US-10-923-379B-1979/c
; Sequence 1979, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1979
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
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; LOCATION: (21)..(21)
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; Query Match 55.0%; Score 11; DB 6; Length 21;
; Best Local Similarity 100.0%; Pred. No. 1.3e+03;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 7 GTTGAAGTTGC 17
; DB 17 GTTGAAGTTGC 7
;
; RESULT 14
US-10-923-379B-2006
; Sequence 2006, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2006
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (3)..(4)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(13)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: internucleotide phosphorothioate linkage
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this
US-10-923-379B-2006
; Query Match 55.0%; Score 11; DB 6; Length 21;
; Best Local Similarity 63.6%; Pred. No. 1.3e+03;
; Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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; DB 2 GUUGAAGUUGC 12
;
; RESULT 15
US-10-923-379B-2007
; Sequence 2007, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
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; SEQ ID NO 2007
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2006
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (3)..(4)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(13)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: internucleotide phosphorothioate linkage
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this
US-10-923-379B-2006
; Query Match 55.0%; Score 11; DB 6; Length 21;
; Best Local Similarity 63.6%; Pred. No. 1.3e+03;
; Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
;
; QY 7 GTTGAAGTTGC 17
; DB 2 GUUGAAGUUGC 12
;
; RESULT 15
US-10-923-379B-2007
; Sequence 2007, Application US/10923379B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Usman, Nassim
; APPLICANT: Haerberli, Peter
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 03-040-D; (400.233)
; CURRENT APPLICATION NUMBER: US/10/923,379B
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 2360
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2007
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc.feature
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; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (10)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (13)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: internucleotide phosphorothioate linkage
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: ribonucleotide unmodified or modified as described for this
; OTHER INFORMATION: sequence
US-10-923-379B-2007
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Query Match 55.0%; Score 11; DB 6; Length 21;
Best Local Similarity 63.6%; Pred. NO. 1.3e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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QY 7 GTTGAAGTTGC 17
Db 3 GUUGAAGUUGC 13
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Search completed: December 3, 2007, 16:25:59
Job time : 206 secs
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GenCore version 6.2.1  
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## OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 16:39:38 ; Search time 457 Seconds

(without alignments)

472.446 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagtgaagtgcgt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 284

Minimum DB seq length: 12

Maximum DB seq length: 30

Post-processing: Minimum Score over Length 70%

Listing first 1000 summaries

## Database :

N Geneseq 200711:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000:\*

4: geneseqn2001a:\*

5: geneseqn2001b:\*

6: geneseqn2002a:\*

7: geneseqn2002b:\*

8: geneseqn2003a:\*

9: geneseqn2003b:\*

10: geneseqn2003c:\*

11: geneseqn2003d:\*

12: geneseqn2004a:\*

13: geneseqn2004b:\*

14: geneseqn2004c:\*

15: geneseqn2004d:\*

16: geneseqn2005a:\*

17: geneseqn2005b:\*

18: geneseqn2005c:\*

19: geneseqn2006a:\*

20: geneseqn2006b:\*

21: geneseqn2006c:\*

22: geneseqn2007:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	over Length	Query Match	Length	ID	Description
1	20	100.0	100.0	20	8	ADA20891 Hu
2	18	90.0	90.0	20	8	ADA20892 Hu
3	15	83.3	75.0	18	8	ADA20832 Hu
C 4	10	83.3	50.0	12	5	ABH71796 Ol
C 5	10	83.3	50.0	12	5	ABH74771 Ol
6	10	83.3	50.0	12	5	ABI53278 Ol
C 7	10	83.3	50.0	12	5	ABI41500 Ol
8	10	83.3	50.0	12	5	ABI10235 Ol
C 9	10	83.3	50.0	12	5	ABI55838 Ol
10	16.4	82.0	82.0	20	8	ADA20946 Mo
11	11.4	81.4	57.0	14	2	AAQ83299 c-
12	16	80.0	80.0	20	8	ABX13068 Hu

13	16	80.0	80.0	20	17	ABD12216
14	16	80.0	80.0	20	19	AEJ97326
15	16	80.0	80.0	20	19	AEK58344 In
C 16	12	80.0	60.0	15	2	AAX75721 Hu
17	10.4	80.0	52.0	13	5	ABF87034 Ol
C 18	10.4	80.0	52.0	13	5	ABF87035 Ol
19	9.4	78.3	47.0	12	5	ABI37784 Ol
C 20	9.4	78.3	47.0	12	5	ABI45117 Ol
C 21	9.4	78.3	47.0	12	5	ABH82576 Ol
C 22	9.4	78.3	47.0	12	5	ABH82576 Ol
23	9.4	78.3	47.0	12	5	ABI29461 Ol
24	9.4	78.3	47.0	12	5	ABI05273 Ol
25	9.4	78.3	47.0	12	5	ABI161450 Ol
C 26	9.4	78.3	47.0	12	5	ABI00657 Ol
C 27	9.4	78.3	47.0	12	5	ABH81979 Ol
C 28	9.4	78.3	47.0	12	5	ABI39385 Ol
29	9.4	78.3	47.0	12	5	ABH80268 Ol
C 30	9.4	78.3	47.0	12	5	ABI14375 Ol
C 31	9.4	78.3	47.0	12	5	ABH75142 Ol
C 32	9.4	78.3	47.0	12	22	AEH30648 E
C 33	17	77.3	85.0	22	22	AEH30671 E
C 34	10	76.9	50.0	13	2	ABV73748 Hu
C 35	10	76.9	50.0	13	2	AAZ21922 Fr
36	10	76.9	50.0	13	5	ABF31261 Ol
C 37	10	76.9	50.0	13	5	ABF71654 Ol
C 38	10	76.9	50.0	13	5	ABF50115 Ol
C 39	10	76.9	50.0	13	5	ABF07779 Ol
40	10	76.9	50.0	13	5	ABC65593 Ol
C 41	10	76.9	50.0	13	5	ABC28727 Ol
C 42	10	76.9	50.0	13	5	ABF71655 Ol
43	10	76.9	50.0	13	5	ABC28726 Ol
44	10	76.9	50.0	13	5	ABC65592 Ol
C 45	10	76.9	50.0	13	5	ABF53415 Ol
46	10	76.9	50.0	13	5	ABF53414 Ol
47	10	76.9	50.0	13	5	ABF31260 Ol
48	10	76.9	50.0	13	5	ABF50114 Ol
49	10	76.9	50.0	13	16	AEQ4526 Hu
50	10	76.9	50.0	13	19	AEH12245 Hu
51	10	76.9	50.0	13	22	AGI70514 Hu
C 52	9	75.0	45.0	12	5	ABI38653 Ol
C 53	9	75.0	45.0	12	5	ABI43950 Ol
54	9	75.0	45.0	12	5	ABI33999 Ol
55	9	75.0	45.0	12	5	ABI69281 Ol
56	9	75.0	45.0	12	5	ABI42808 Ol
57	9	75.0	45.0	12	5	ABH72541 Ol
58	9	75.0	45.0	12	5	ABH88159 Ol
59	9	75.0	45.0	12	5	ABH98609 Ol
60	9	75.0	45.0	12	5	ABI37700 Ol
61	9	75.0	45.0	12	5	ABI79970 Ol
62	9	75.0	45.0	12	5	ABH98752 Ol
63	9	75.0	45.0	12	5	ABI10039 Ol
64	9	75.0	45.0	12	5	ABI19673 Ol
C 65	9	75.0	45.0	12	5	ABH81377 Ol
C 66	9	75.0	45.0	12	5	ABI65921 Ol
C 67	9	75.0	45.0	12	5	ABI32591 Ol
C 68	9	75.0	45.0	12	5	ABH84637 Ol
C 69	9	75.0	45.0	12	5	ABI45848 Ol
C 70	9	75.0	45.0	12	5	ABI08021 Ol
71	9	75.0	45.0	12	5	ABI58136 Ol
72	9	75.0	45.0	12	5	ABH99938 Ol
C 73	9	75.0	45.0	12	5	ABI38557 Ol
C 74	9	75.0	45.0	12	5	ABI60242 Ol
C 75	9	75.0	45.0	12	5	ABI05053 Ol
C 76	9	75.0	45.0	12	5	ABI69662 Ol
C 77	9	75.0	45.0	12	6	ABK72546 Hu
78	9	75.0	45.0	14	2	AAX34784 Ne
C 79	10.4	74.3	52.0	13	5	ABC61646 Ol
80	9.6	73.8	48.0	13	5	ABC61647 Ol
C 81	9.6	73.8	48.0	13	5	ABC61647 Ol
C 82	11	73.3	55.0	15	2	AAX75746 Hu
C 83	11	73.3	55.0	15	3	Aaz64449 Su
C 84	11	73.3	55.0	15	6	ABE76210 He
C 85	11	73.3	55.0	15	6	ABX01502 He

c 86	11	73.3	55.0	15	8	ABQ77353	Abq77353 Re	c 159	8.4	70.0	42.0	12	2	AAT93676	AA93676 Ex
c 87	8.8	73.3	44.0	12	2	AAQ88636	AAQ88636 Hu	c 160	8.4	70.0	42.0	12	2	AAV42278	AAV42278 Cl
c 88	8.8	73.3	44.0	12	2	AAQ88635	AAQ88635 Hu	c 161	8.4	70.0	42.0	12	2	AAV42254	AAV42254 Cl
c 89	8.8	73.3	44.0	12	4	AAZ30061	Sp	c 162	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 90	8.8	73.3	44.0	12	4	AAZ31364	In	c 163	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 91	8.8	73.3	44.0	12	4	AAZ02762	Hu	c 164	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 92	8.8	73.3	44.0	12	5	ABH93674	Hu	c 165	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 93	8.8	73.3	44.0	12	5	ABH93674	Hu	c 166	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 94	8.8	73.3	44.0	12	5	ABH93674	Hu	c 167	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 95	8.8	73.3	44.0	12	5	ABH93674	Hu	c 168	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 96	8.8	73.3	44.0	12	5	ABH93674	Hu	c 169	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 97	8.8	73.3	44.0	12	5	ABH93674	Hu	c 170	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 98	8.8	73.3	44.0	12	5	ABH93674	Hu	c 171	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 99	8.8	73.3	44.0	12	5	ABH93674	Hu	c 172	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 100	8.8	73.3	44.0	12	5	ABH93674	Hu	c 173	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 101	8.8	73.3	44.0	12	5	ABH93674	Hu	c 174	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 102	8.8	73.3	44.0	12	5	ABH93674	Hu	c 175	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 103	8.8	73.3	44.0	12	5	ABH93674	Hu	c 176	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 104	8.8	73.3	44.0	12	8	AAU52648	Hu	c 177	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 105	8.8	73.3	44.0	12	17	AEC62435	Hu	c 178	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 106	8.8	73.3	44.0	12	17	AEC62417	Hu	c 179	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 107	8.8	73.3	44.0	12	17	AEC62419	Hu	c 180	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 108	8.8	73.3	44.0	12	19	AELO3638	Hu	c 181	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 109	8.8	73.3	44.0	12	19	AELO3639	Hu	c 182	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 110	8.8	73.3	44.0	12	22	AELO3631	E.	c 183	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 111	8.8	73.3	44.0	12	22	AGD66526	Hu	c 184	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 112	12.4	72.9	62.0	17	3	AAU5403	Ha	c 185	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 113	12.4	72.9	62.0	17	3	AAU5403	Ha	c 186	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 114	16	72.7	80.0	22	19	AEB24548	BA	c 187	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 115	16	72.7	80.0	22	19	AEB24548	BA	c 188	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 116	16	72.7	80.0	22	19	AEB24548	BA	c 189	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 117	9.4	72.3	47.0	13	5	ABH93674	Ol	c 190	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 118	9.4	72.3	47.0	13	5	ABH93674	Ol	c 191	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 119	9.4	72.3	47.0	13	5	ABH93674	Ol	c 192	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 120	9.4	72.3	47.0	13	5	ABH93674	Ol	c 193	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 121	9.4	72.3	47.0	13	5	ABH93674	Ol	c 194	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 122	9.4	72.3	47.0	13	5	ABH93674	Ol	c 195	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 123	9.4	72.3	47.0	13	5	ABH93674	Ol	c 196	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 124	9.4	72.3	47.0	13	5	ABH93674	Ol	c 197	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 125	9.4	72.3	47.0	13	5	ABH93674	Ol	c 198	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 126	9.4	72.3	47.0	13	5	ABH93674	Ol	c 199	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 127	9.4	72.3	47.0	13	5	ABH93674	Ol	c 200	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 128	9.4	72.3	47.0	13	5	ABH93674	Ol	c 201	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 129	9.4	72.3	47.0	13	5	ABH93674	Ol	c 202	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 130	9.4	72.3	47.0	13	5	ABH93674	Ol	c 203	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 131	9.4	72.3	47.0	13	5	ABH93674	Ol	c 204	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 132	9.4	72.3	47.0	13	5	ABH93674	Ol	c 205	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 133	9.4	72.3	47.0	13	5	ABH93674	Ol	c 206	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 134	9.4	72.3	47.0	13	5	ABH93674	Ol	c 207	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 135	9.4	72.3	47.0	13	5	ABH93674	Ol	c 208	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 136	9.4	72.3	47.0	13	5	ABH93674	Ol	c 209	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 137	9.4	72.3	47.0	13	5	ABH93674	Ol	c 210	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 138	9.4	72.3	47.0	13	5	ABH93674	Ol	c 211	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 139	9.4	72.3	47.0	13	5	ABH93674	Ol	c 212	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 140	9.4	72.3	47.0	13	5	ABH93674	Ol	c 213	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 141	9.4	72.3	47.0	13	5	ABH93674	Ol	c 214	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 142	9.4	72.3	47.0	13	5	ABH93674	Ol	c 215	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 143	9.4	72.3	47.0	13	5	ABH93674	Ol	c 216	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 144	9.4	72.3	47.0	13	5	ABH93674	Ol	c 217	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 145	9.4	72.3	47.0	13	5	ABH93674	Ol	c 218	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 146	9.4	72.3	47.0	13	5	ABH93674	Ol	c 219	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 147	9.4	72.3	47.0	13	5	ABH93674	Ol	c 220	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 148	9.4	72.3	47.0	13	13	ADR35833	Hu	c 221	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 149	9.4	72.3	47.0	13	13	ADR35834	Hu	c 222	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 150	9.4	72.3	47.0	13	13	ADR35835	Hu	c 223	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 151	12.2	71.8	61.0	17	13	ADR35832	Hu	c 224	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 152	10	71.4	50.0	14	2	AAQ83300	C-	c 225	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 153	17	70.8	85.0	24	19	AEU10477	Ta	c 226	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 154	17	70.8	85.0	24	19	AEU10484	Ta	c 227	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 155	10.6	70.7	53.0	15	6	ABS64186	Ta	c 228	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 156	12	70.6	60.0	17	2	AAU71130	Hu	c 229	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 157	12	70.6	60.0	17	2	AAU71129	Hu	c 230	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol
c 158	12	70.6	60.0	17	8	ABE61076	Hu	c 231	8.4	70.0	42.0	12	5	ABH93674	ABH93674 Ol

232	8.4	70.0	42.0	12	5	ABI00465	Abi00465 Ol
233	8.4	70.0	42.0	12	5	ABH99246	Abh99246 Ol
C 234	8.4	70.0	42.0	12	5	ABH88414	Abh88414 Ol
C 235	8.4	70.0	42.0	12	5	ABI66132	Abi66132 Ol
C 236	8.4	70.0	42.0	12	5	ABI67005	Abi67005 Ol
237	8.4	70.0	42.0	12	5	ABI67274	Abi67274 Ol
C 238	8.4	70.0	42.0	12	5	ABI52749	Abi52749 Ol
C 239	8.4	70.0	42.0	12	5	ABI16623	Abi16623 Ol
240	8.4	70.0	42.0	12	5	ABI44330	Abi44330 Ol
241	8.4	70.0	42.0	12	5	ABI61490	Abi61490 Ol
242	8.4	70.0	42.0	12	5	ABI74887	Abi74887 Ol
243	8.4	70.0	42.0	12	5	ABI10236	Abi10236 Ol
C 244	8.4	70.0	42.0	12	5	ABI31459	Abi31459 Ol
C 245	8.4	70.0	42.0	12	5	ABI32242	Abi32242 Ol
246	8.4	70.0	42.0	12	5	ABI69897	Abi69897 Ol
C 247	8.4	70.0	42.0	12	5	ABH92665	Abh92665 Ol
C 248	8.4	70.0	42.0	12	5	ABI29165	Abi29165 Ol
C 249	8.4	70.0	42.0	12	5	ABI22105	Abi22105 Ol
250	8.4	70.0	42.0	12	5	ABH97330	Abh97330 Ol
C 251	8.4	70.0	42.0	12	5	ABI02630	Abi02630 Ol
252	8.4	70.0	42.0	12	5	ABH84497	Abh84497 Ol
C 253	8.4	70.0	42.0	12	5	ABI38801	Abi38801 Ol
C 254	8.4	70.0	42.0	12	5	ABI62796	Abi62796 Ol
255	8.4	70.0	42.0	12	5	ABI64102	Abi64102 Ol
C 256	8.4	70.0	42.0	12	5	ABH92662	Abh92662 Ol
C 257	8.4	70.0	42.0	12	5	ABI18502	Abi18502 Ol
C 258	8.4	70.0	42.0	12	5	ABI47133	Abi47133 Ol
C 259	8.4	70.0	42.0	12	5	ABI41721	Abi41721 Ol
C 260	8.4	70.0	42.0	12	5	ABI42212	Abi42212 Ol
C 261	8.4	70.0	42.0	12	5	ABI61765	Abi61765 Ol
C 262	8.4	70.0	42.0	12	5	ABI67350	Abi67350 Ol
263	8.4	70.0	42.0	12	5	ABI80116	Abi80116 Ol
C 264	8.4	70.0	42.0	12	5	ABH69990	Abh69990 Ol
265	8.4	70.0	42.0	12	5	ABH95291	Abh95291 Ol
266	8.4	70.0	42.0	12	5	ABH98049	Abh98049 Ol
C 267	8.4	70.0	42.0	12	5	ABI33882	Abi33882 Ol
C 268	8.4	70.0	42.0	12	5	ABI41817	Abi41817 Ol
C 269	8.4	70.0	42.0	12	5	ABI48505	Abi48505 Ol
C 270	8.4	70.0	42.0	12	5	ABI76925	Abi76925 Ol
271	8.4	70.0	42.0	12	5	ABI72013	Abi72013 Ol
C 272	8.4	70.0	42.0	12	5	ABI58229	Abi58229 Ol
C 273	8.4	70.0	42.0	12	5	ABI52907	Abi52907 Ol
C 274	8.4	70.0	42.0	12	5	ABI64624	Abi64624 Ol
C 275	8.4	70.0	42.0	12	5	ABI62006	Abi62006 Ol
C 276	8.4	70.0	42.0	12	5	ABI17895	Abi17895 Ol
C 277	8.4	70.0	42.0	12	5	ABH94593	Abh94593 Ol
C 278	8.4	70.0	42.0	12	5	ABH96494	Abh96494 Ol
279	8.4	70.0	42.0	12	5	ABI39317	Abi39317 Ol
C 280	8.4	70.0	42.0	12	5	ABI52789	Abi52789 Ol
C 281	8.4	70.0	42.0	12	5	ABI47624	Abi47624 Ol
C 282	8.4	70.0	42.0	12	5	ABI77409	Abi77409 Ol
C 283	8.4	70.0	42.0	12	5	ADD69888	Le
C 284	8.4	70.0	42.0	12	22	AER38463	Li

## ALIGNMENTS

RESULT 1  
ADAZ0891  
ID ADAZ0891 standard; DNA; 20 BP.  
XX AC ADAZ0891;  
XX DT 20-NOV-2003 (first entry)  
XX DE Human BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:64.  
XX KW BCL2-associated X; BAX; nootropic; neuroprotective; antiparkinsonian;  
XX KW anticonvulsant; ophthalmological; antidiabetic; virocidic;  
KW antisense therapy; BAX antagonist; BAX inhibitor;  
KW familial amyotrophic lateral sclerosis; Alzheimer's disease;  
KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;

Query Match 100.0%; Score 20; DB 8; Length 20;  
Score over Length 100.0%;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW diabetes-associated ocular disorder; scrapie infection;  
KW aberrant apoptosis; human; phosphorothioate; ss.  
XX Synthetic.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FT modified\_base 1..20  
FT /mod\_base= OTHER  
FT /tag= b  
FT /note= "phosphorothioate linkages, and all cytidine  
modified\_base 1..5  
FT residues are 5-methylcytidines"  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX WO2003008543-A2.  
PN 30-JAN-2003.  
PD 13-JUL-2002; 2002WO-US022417.  
XX 17-JUL-2001; 2001US-00908147.  
XX (ISIS-) ISIS PHARM INC.  
XX Zhang H, Watt AT;  
XX WPI; 2003-239321/23.  
XX New antisense compounds, useful for modulating the expression of BCL2-  
associated X (BAX) protein or for treating a disease or condition  
associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease  
or Alzheimer's disease.  
PS Claim 3; Page 86; 139pp; English.

CC The present invention describes a compound (I) 8-50 nucleobases in length  
targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)  
protein, where the compound specifically hybridizes with the nucleic acid  
molecule encoding BAX protein and inhibits the expression of BAX protein.  
CC The compound specifically hybridizes with at least 8-nucleobase portion  
of an active site on a nucleic acid molecule encoding BAX protein. Also  
described: (1) a composition comprising (I) and a pharmaceutical carrier  
or diluent; (2) inhibiting the expression of BAX protein in cells or  
tissues comprising contacting the cells or tissues with (I); and (3)  
treating an animal having a disease or condition associated with BAX  
protein comprising administering to the animal (I) so that expression of  
BAX protein is inhibited. (I) has nootropic, neuroprotective,  
antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and  
virocidic activities, and can be used in antisense therapy, and as a BAX  
antagonist. The antisense compounds (I) are useful for modulating the  
expression of BAX protein, and for treating a disease or condition  
associated with BAX protein, e.g. familial amyotrophic lateral  
sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,  
cartilage-hair hyperplasia, diabetes-associated ocular disorders or  
scrapie infection, or a condition that arises from aberrant apoptosis.  
CC The compounds are useful as research reagents and in diagnostics. The  
present sequence represents a human BAX chimeric phosphorothioate  
oligonucleotide, which is used in an example from the present invention.

XX Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

QY 1 GCCCCAGTTGAAGTGGCCGT 20  
 DB 1 GCCCCAGTTGAAGTGGCCGT 20

RESULT 2  
 ID ADA20892 standard; DNA; 20 BP.  
 AC ADA20892;  
 XX 20-NOV-2003 (first entry)  
 XX Human BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:65.

XX BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;  
 KW anticonvulsant; ophthalmological; antidiabetic; virucide;  
 KW antisense therapy; BAX antagonist; BAX inhibitor;  
 KW familial amyotrophic lateral sclerosis; Alzheimer's disease;  
 KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;  
 KW diabetes-associated ocular disorder; scrapie infection;  
 KW aberrant apoptosis; human; phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FT modified\_base 1..20 /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages, and all cytidine  
 residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 XX  
 PN WO2003008543-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 13-JUL-2002; 2002WO-US022417.  
 XX  
 PR 17-JUL-2001; 2001US-00908147.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Zhang H, Watt AT;  
 XX  
 DR WPI; 2003-239321/23.  
 XX  
 XX New antisense compounds, useful for modulating the expression of BCL2-  
 associated X (BAX) protein or for treating a disease or condition  
 associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease  
 or Alzheimer's disease.  
 XX  
 PS Claim 3; Page 86; 139pp; English.  
 XX

The present invention describes a compound (I) 8-50 nucleobases in length  
 targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)  
 protein, where the compound specifically hybridises with the nucleic acid  
 molecule encoding BAX protein and inhibits the expression of BAX protein.  
 The compound specifically hybridises with at least 8-nucleobase portion  
 of an active site on a nucleic acid molecule encoding BAX protein. Also  
 described: (1) a composition comprising (I) and a pharmaceutical carrier  
 or diluent; (2) inhibiting the expression of BAX protein in cells or  
 tissues comprising contacting the cells or tissues with (I); and (3)  
 treating an animal having a disease or condition associated with BAX  
 protein comprising administering to the animal (I) so that expression of

CC BAX protein is inhibited. (I) has neurotropic, neuroprotective,  
 CC antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and  
 CC virucide activities, and can be used in antisense therapy, and as a BAX  
 CC antagonist. The antisense compounds (I) are useful for modulating the  
 CC expression of BAX protein, and for treating a disease or condition  
 CC associated with BAX protein, e.g. familial amyotrophic lateral  
 CC sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,  
 CC cartilage-hair hyperplasia, diabetes-associated ocular disorders or  
 CC scrapie infection, or a condition that arises from aberrant apoptosis.  
 CC The compounds are useful as research reagents and in diagnostics. The  
 CC present sequence represents a human BAX chimeric phosphorothioate  
 CC oligonucleotide, which is used in an example from the present invention.  
 XX  
 SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 8; Length 20;  
 Score over Length 90.0%;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTGGCC 18  
 |||||  
 DB 3 GCCCCAGTTGAAGTGGCC 20

RESULT 3  
 ADA20832  
 ID ADA20832 standard; DNA; 18 BP.  
 XX ADA20832;  
 AC ADA20832;  
 XX 20-NOV-2003 (first entry)  
 DT Human BCL2-associated X protein reverse PCR primer SEQ ID NO:5.

DE BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;  
 KW anticonvulsant; ophthalmological; antidiabetic; virucide;  
 KW antisense therapy; BAX antagonist; BAX inhibitor;  
 KW familial amyotrophic lateral sclerosis; Alzheimer's disease;  
 KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;  
 KW diabetes-associated ocular disorder; scrapie infection;  
 KW aberrant apoptosis; human; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.

XX WO2003008543-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 13-JUL-2002; 2002WO-US022417.  
 XX  
 PR 17-JUL-2001; 2001US-00908147.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Zhang H, Watt AT;  
 XX  
 DR WPI; 2003-239321/23.  
 XX  
 XX New antisense compounds, useful for modulating the expression of BCL2-  
 associated X (BAX) protein or for treating a disease or condition  
 associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease  
 or Alzheimer's disease.  
 XX  
 PS Example 13; Page 82; 139pp; English.  
 XX

The present invention describes a compound (I) 8-50 nucleobases in length  
 targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)  
 protein, where the compound specifically hybridises with the nucleic acid  
 molecule encoding BAX protein and inhibits the expression of BAX protein.  
 The compound specifically hybridises with at least 8-nucleobase portion  
 of an active site on a nucleic acid molecule encoding BAX protein. Also  
 described: (1) a composition comprising (I) and a pharmaceutical carrier  
 or diluent; (2) inhibiting the expression of BAX protein in cells or  
 tissues comprising contacting the cells or tissues with (I); and (3)  
 treating an animal having a disease or condition associated with BAX  
 protein comprising administering to the animal (I) so that expression of



described: (1) a composition comprising (I) and a pharmaceutical carrier or diluent; (2) inhibiting the expression of BAX protein in cells or tissues comprising contacting the cells or tissues with (I); and (3) treating an animal having a disease or condition associated with BAX protein comprising administering to the animal (I) so that expression of BAX protein is inhibited. (I) has neurotropic, neuroprotective, antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and virucide activities, and can be used in antineoplastic, antidiabetic and antagonist. The antisense compounds (I) are useful for modulating the expression of BAX protein, and for treating a disease or condition associated with BAX protein, e.g. familial amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease, cartilage-hair hyperplasia, diabetes-associated ocular disorders or scrapie infection, or a condition that arises from aberrant apoptosis. The compounds are useful as research reagents and in diagnostics. The present sequence represents a PCR primer for the human BAX protein, which is used in an example from the present invention.

Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 8; Length 18;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTT 15  
| | | | | | | | | |  
Db 4 GCCCCAGTTGAAGTT 18

## RESULT 4

ABH71796/c  
ID ABH71796 standard; DNA; 12 BP.

AC ABH71796;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 271773 for detecting SNP TSC0002613.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 271773; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 5; Length 12;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
| | | | | | | | | |  
Db 10 AGTTGAAGTT 1

## RESULT 5

ABH74771/c

ID ABH74771 standard; DNA; 12 BP.

XX ABH74771;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 274756 for detecting SNP TSC0003668.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 274756; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 5; Length 12;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 7.2e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





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PR 17-JUL-2001; 2001US-00908147.
XX (ISIS-) ISIS PHARM INC.
XX Zhang H, Watt AT;
XX WPI; 2003-239321/23.
XX
XX New antisense compounds, useful for modulating the expression of BCL2-
PT associated X (BAX) protein or for treating a disease or condition
PT associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
PT or Alzheimer's disease.
XX
XX Claim 3; Page 93; 139pp; English.
XX
XX The present invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
CC protein, where the compound specifically hybridizes with the nucleic acid
CC molecule encoding BAX protein and inhibits the expression of BAX protein.
CC The compound specifically hybridizes with at least 8-nucleobase portion
CC of an active site on a nucleic acid molecule encoding BAX protein. Also
CC described: (1) a composition comprising (I) and a pharmaceutical carrier
CC or diluent; (2) inhibiting the expression of BAX protein in cells or
CC tissues comprising contacting the cells or tissues with (I); and (3)
CC treating an animal having a disease or condition associated with BAX
CC protein comprising administering to the animal (I) so that expression of
CC BAX protein is inhibited. (I) has neurotropic, neuroprotective,
CC antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
CC virucide activities, and can be used in antisense therapy, and as a BAX
CC antagonist. The antisense compounds (I) are useful for modulating the
CC expression of BAX protein, and for treating a disease or condition
CC associated with BAX protein, e.g. familial amyotrophic lateral
CC sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
CC cartilage-hair hyperplasia, diabetes-associated ocular disorders or
CC scrapie infection, or a condition that arises from aberrant apoptosis.
CC The compounds are useful as research reagents and in diagnostics. The
CC present sequence represents a mouse BAX chimeric phosphorothioate
CC oligonucleotide, which is used in an example from the present invention.
XX
XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match 82.0%; Score 16.4; DB 8; Length 20;
Score over Length 82.0%;
Best Local Similarity 94.4%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCCGT 20
Db 1 CCCAGTTGAAGTTGCCAT 18

RESULT 11
AAQ83299
ID AAQ83299 standard; DNA; 14 BP.
XX
XX AAQ83299;
AC
XX
XX 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
PR
DE c-jun antisense oligonucleotide.
XX
XX c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
KW phosphorothioate; ss.
XX
XX Synthetic.
OS
XX WO9502051-A2.
PN
XX 19-JAN-1995.
XX
XX 06-JUL-1994; 94WO-EP002218.
XX

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PR 10-JUL-1993; 93EP-00111059.
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;
XX WPI; 1995-066896/09.
XX
XX Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and
PT treating neuronal injury, degeneration, cell death and/or neoplasms.
XX
XX Claim 2; Page 30; 86pp; English.
XX
XX Antisense nucleic acid hybridizing with an area of the mRNA and/or DNA
CC comprising the genes c-jun, jun-B or c-fos, expression of which plays a
CC causal role in neuronal injury, degeneration, cell death and/or
CC neoplasms, can be used to prevent and treat such conditions. c-jun
CC antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B
CC antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-
CC fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.
CC Preferably the antisense sequences are phosphorothioate oligonucleotides
CC since these are not destroyed as fast by endogenous factors as naturally
CC occurring molecules. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 14 BP; 2 A; 1 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 57.0%; Score 11.4; DB 2; Length 14;
Score over Length 81.4%;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCG 19
Db 2 GTTGAAGTTGCTG 14

RESULT 12
ABX13068
ID ABX13068 standard; DNA; 20 BP.
XX
XX ABX13068;
AC
XX
XX 29-MAY-2003 (first entry)
DT
XX
XX Human bax PCR primer #2.
DE
XX
XX Human; insulin-like growth factor binding protein 5; IGFBP-5; primer; ss;
KW cytostatic; apoptosis; cancer; breast; prostate; ovary; lung; colon; PCR;
KW bax.
XX
XX Homo sapiens.
OS
XX WO2003006029-A1.
PN
XX 23-JAN-2003.
XX
XX 15-JUL-2002; 2002WO-AU000936.
XX
XX 13-JUL-2001; 2001AU-00006331.
PR
XX (UNSY ) UNIV SYDNEY.
XX
XX Baxter RC, Butt AJ;
XX WPI; 2003-221646/21.
XX
XX Inducing apoptosis in cancer cell, useful for treating cancer, e.g.
PT breast or prostate cancer comprises increasing the expression of insulin-
PT like growth factor binding protein-5 (IGFBP-5) by the cell to an
PT apoptosis-inducing amount.
XX
XX Example; Page 29; 65pp; English.
XX

```

CC The invention relates to a method for inducing apoptosis in a cancer cell  
CC comprising increasing the expression of insulin-like growth factor  
CC binding protein 5 (IGFBP-5) by the cell to an apoptosis-inducing amount.  
CC The invention also relates to a method of sensitizing a cancer cell to  
CC stimuli that induce apoptosis by increasing the expression of IGFBP-5 by  
CC the cell, a method of killing a cancer cell by sensitizing the cell to  
CC stimuli that induce apoptosis and simultaneously exposing the cell to  
CC apoptosis-inducing stimuli, or exposing the cell to apoptosis-inducing  
CC stimuli and simultaneously or subsequently increasing the expression of  
CC IGFBP-5 by the cell to an apoptosis-inducing amount. The methods are  
CC useful for treating cancer, such as breast, prostate, ovarian, lung or  
CC colon cancer, by inducing apoptosis or killing cancer cells. This  
CC sequence represents a bax PCR primer used in the method of the invention  
XX  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 8; Length 20;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20  
Db 1 CAGTTGAAGTTGCCGT 16  
|||||

RESULT 13  
AED12216  
ID AED12216 standard; DNA; 20 BP.

XX  
XX  
AC AED12216;

DT 01-DEC-2005 (first entry)

DE Bax (human) RT-PCR primer SEQ ID 16.

XX Drug screening; apoptosis; protein interaction; Bax; Cytostatic;  
KW Neuroprotective; cancer; neurodegenerative disease; ss; RT-PCR;  
KW reverse transcriptase PCR; primer.

XX Homo sapiens.

XX WO2005093082-A1.

XX 06-OCT-2005.

XX 23-MAR-2005; 2005WO-JP005247.

XX 26-MAR-2004; 2004JP-00093266.

XX 14-JUN-2004; 2004JP-00176107.

XX (HISM ) HISAMITSU PHARM CO LTD.  
XX (CHIB-) CHIBA PREFECTURE.

XX Nakagawara A, Ozaki T;

XX WPI; 2005-713863/73.

XX Screening compound capable of stimulating or inhibiting apoptosis,  
PT involves judging compound capable of intensifying interaction between p73  
PT and IKK-alpha as compound capable of stimulating or inhibiting apoptosis.

XX Example; SEQ ID NO 16; 79pp; Japanese.

XX The invention relates to screening (M1) a compound capable of stimulating  
CC or inhibiting apoptosis, comprising identifying a compound capable of  
CC modulating the interaction between p73 and IKK-alpha (IkappaB kinase) as  
CC a compound capable of stimulating or inhibiting apoptosis. The method  
CC comprise culturing a cell that expresses p73 and IKK-alpha in the  
CC presence or absence of test compound, measuring an interaction between  
CC p73 and IKK-alpha in each cultured cell and judging a compound as being  
CC capable of stimulating or inhibiting apoptosis, when an interaction  
CC between p73 and IKK-alpha in the cell cultured in the presence of test

CC compound, is stronger or weaker, in comparison to cell cultured in the  
CC absence of test compound, respectively. Also included are an apoptosis  
CC stimulator comprising AED12224 (human IKK-alpha, or a nucleic acid that  
CC encodes human IKK-alpha) and an apoptosis inhibitor fusion degradation  
CC alpha K44A mutant (AED12225) or human ubiquitin fusion degradation  
CC protein-2a (AED12226). The method is useful for screening a compound  
CC capable of stimulating or inhibiting apoptosis utilized for treating  
CC cancer or neurodegenerative diseases. The present sequence is an RT-PCR  
CC primer for a non-IKK mRNA (i.e. is either a control or is for an IKK  
CC binding protein).

XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 17; Length 20;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20

Db 1 CAGTTGAAGTTGCCGT 16  
|||||

RESULT 14

AEJ97326

ID AEJ97326 standard; DNA; 20 BP.

XX  
XX  
AC AEJ97326;

DT 02-NOV-2006 (first entry)

DE RT-PCR primer BAX reverse, SEQ ID 8.

XX Therapeutic; apoptosis inhibition; apoptosis stimulation; neoplasm;  
KW cancer; neurodegenerative disease; neurological disorder; RT-PCR; primer;  
KW ss.

XX Homo sapiens.

XX JP2006223265-A.

XX 31-AUG-2006.

XX 21-FEB-2005; 2005JP-00044554.

XX 21-FEB-2005; 2005JP-00044554.

XX (HISM ) HISAMITSU PHARM CO LTD.  
XX (CHIB-) CHIBA PREFECTURE.

XX Nakagawara A, Ozaki T;

XX WPI; 2006-590511/51.

XX Screening compound capable of promoting or suppressing apoptosis, for  
PT treating cancer or neurodegenerative disease, involves determining  
PT whether compound inhibits or enhances interaction of p53 and NFBD1.

XX Example; SEQ ID NO 8; 21pp; Japanese.

XX The invention relates to the screening of a compound capable of promoting  
CC or suppressing apoptosis. The method comprises determining whether a  
CC compound inhibits or enhances the interaction of p53 and NFBD1 (nuclear  
CC factor with BCR domains protein 1), or culturing a cell expressing p53  
CC and NFBD1 in the presence and in the absence of a test compound and  
CC measuring the interaction of p53 and NFBD1 in a cultured cell. Further  
CC disclosed is an apoptosis inhibitor with p53 binding activity having an  
CC amino acid sequence as given in AEJ97331. The method is useful for  
CC screening a compound that promotes or suppresses apoptosis and is useful  
CC as a therapeutic agent for cancer and neurodegenerative disorders. The  
CC current sequence represents an RT-PCR primer used in an exemplification  
CC of the invention.

SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 19; Length 20;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CAGTTGAAGTTGCCGT 20  
|||||  
DB 1 CAGTTGAAGTTGCCGT 16

RESULT 15  
AEK58344  
ID AEK58344 standard; DNA; 20 BP.  
XX AEK58344;  
AC AEK58344;

XX 16-NOV-2006 (first entry)  
DE Interferon-related gene specific PCR primer, SEQ ID NO:21.  
XX screening; gene expression; hepatitis C virus infection;  
KW antinflammatory; hepatotropic; virucide; gastrointestinal disease;  
KW infection; diagnostic; diagnosis; liver cirrhosis; inflammation;  
KW microarray; DNA amplification; therapeutic; ss; primer; PCR; interferon.  
XX Homo sapiens.  
XX OS  
XX PN WO2006085407-A1.  
XX PD 17-AUG-2006.  
XX 30-SEP-2005; 2005WO-JP018573.  
XX 09-FEB-2005; 2005JP-00033707.  
XX (UYN1-) UNIV NIPPON.  
XX PA  
XX PI Esumi M, Takayama T;  
XX WPI; 2006-680124/70.  
XX Screening gene whose expression is increased in high/low hepatitis C  
PT virus (HCV) tissue, involves selecting gene based on its expression level  
PT in low and high virus group tissues being selected based on HCV 18SrRNA  
PT analysis.  
XX Example 1; SEQ ID NO 21; 75pp; Japanese.  
XX The new invention relates to screening a gene whose expression is  
CC increased in high hepatitis C virus (HCV) group tissue or low HCV group  
CC tissue. The method involves selecting liver tissue whose value is  
CC obtained by dividing copy number of HCV per 50 ng of liver tissue-derived  
CC cDNA by the value of 18S-RNA is not more than 300 units as low virus  
CC group tissue and not more than 30000 units as high virus group tissue,  
CC measuring gene expression level in tissues, and selecting gene whose  
CC expression is increased in high/low virus group tissue more than low/high  
CC virus group tissue. Also described is a diagnostic of diseases relevant  
CC to viral load, comprising (a) gene (e.g. OASL, EHF, CXCL6, IRS2, MAP1B  
CC and CXCL10) with a sequence of one of SEQ ID No. 54-131, where the  
CC expression of the gene enhances in high virus group, (b) gene (e.g.  
CC FLJ4615, 28S rRNA, ENCL1, RAP81, BAGE and PSMA8) comprising a sequence of  
CC one of SEQ ID No. 132-170, where the expression of the gene enhances in  
CC low virus group, (c) one of gene (e.g. HLA-DQA1, TMPSR52, SPEC2, SNA12,  
CC IFI44, LEPR and FNB31) of CHH gene cluster comprising a sequence of SEQ  
CC ID No. 171-237, where the expression of the gene enhances in high virus  
CC group of chronic hepatitis, (d) one of gene (e.g. FLJ46154, KCNN2, CRP,  
CC LOC334145 and HMG2) of CHL gene cluster comprising a sequence of SEQ ID  
CC No. 238-258, where the expression of the gene enhances in low virus group  
CC of chronic hepatitis, (e) one of gene (e.g. SDS, GIP2, KLF6, ZDHHC11,  
CC GAD645D, MX1 and BCL3) of LCH gene cluster comprising a sequence of one  
CC of SEQ ID No. 259-285, where the expression of the gene enhances in high

CC virus group of liver cirrhosis, or (f) one of gene (e.g. MND4, CLCSF12,  
CC SLC8A1, PST, API52, LARS and TBC1D1) of LCU gene cluster comprising a  
CC sequence of one of SEQ ID No. 286-302, where the expression of the gene  
CC enhances in low virus group of liver cirrhosis. The measurement of  
CC expression is carried out using microarray and/or real-time PCR. The  
CC method is useful for screening a gene whose expression is increased in a  
CC high virus group tissue containing a large amount of HCV or in a low  
CC virus group tissue containing small amount of HCV, for development of  
CC therapeutic agent of HCV. This sequence is a primer for PCR amplification  
CC of an interferon-related gene, useful in the new method of the invention.  
XX  
XX SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 19; Length 20;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CAGTTGAAGTTGCCGT 20  
|||||  
DB 1 CAGTTGAAGTTGCCGT 16

RESULT 16  
AAK75721/c  
ID AAK75721 standard; RNA; 15 BP.  
XX AAK75721;  
AC AAK75721;  
XX 28-JUL-1999 (first entry)  
DE Human flt-1 and KDR hammerhead ribozyme target site #55.  
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.  
XX Homo sapiens.  
XX OS  
XX PN WO9715662-A2.  
XX 01-MAY-1997.  
XX 25-OCT-1996; 96WO-US017480.  
XX 26-OCT-1995; 95US-0005974P.  
XX 11-JAN-1996; 96US-000584040.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (CHIR) CHIRON CORP.  
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
XX WPI; 1997-259017/23.  
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX Example 9; Page 191; 218pp; English.  
XX The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
CC of nucleic acid molecules from the present invention

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XX SQ Sequence 15 BP; 3 A; 3 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 60.0%; Score 12; DB 2; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 17
ABF87034
ID ABF87034 standard; DNA; 13 BP.
AC ABF87034;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 187031 for detecting SNP TSC0046102.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR 18-OCT-2001.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 187031; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 52.0%; Score 10.4; DB 5; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 4.6e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 1 AGTTGAAGTTGC 12

RESULT 18
ABF87035/C
ID ABF87035 standard; DNA; 13 BP.
XX
AC ABF87035;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 187032 for detecting SNP TSC0046102.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR 18-OCT-2001.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 187032; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 52.0%; Score 10.4; DB 5; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 4.6e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17
Db 13 AGTTGAAGTTGC 2

RESULT 19
ABI37784
ID ABI37784 standard; DNA; 12 BP.
XX
AC ABI37784;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 337757 for detecting SNP TSC0004732.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
```



KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 337757; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
SQ Query Match 47.0%; Score 9.4; DB 5; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
Db 1 AGTAGAAGTTG 11  
RESULT 20  
ABI45117/c  
ID ABI45117 standard; DNA; 12 BP.  
XX ABI45117;  
AC ABI45117;  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 345090 for detecting SNP TSC0043868.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
PR

XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 345090; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
SQ Query Match 47.0%; Score 9.4; DB 5; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
Db 11 AGTTGAGTTG 11  
RESULT 21  
ABH82576/c  
ID ABH82576 standard; DNA; 12 BP.  
XX ABH82576;  
AC ABH82576;  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 282569 for detecting SNP TSC0010870.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 282569; 29pp + Sequence Listing; German.



XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16  
Db 12 AGTTGAGTTG 2  
|||||

RESULT 22  
ABI29461  
ID ABI29461 standard; DNA; 12 BP.  
XX  
AC ABI29461;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 329434 for detecting SNP TSC0034943.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 329434; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16  
Db 1 AGTAGAAGTTG 11  
|||||

RESULT 23  
ABI05273  
ID ABI05273 standard; DNA; 12 BP.  
XX  
AC ABI05273;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 305246 for detecting SNP TSC0021354.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 305246; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16  
Db 2 AGTTGAGTTG 12  
|||||



```
PR 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
PS Claim 1; SEQ ID NO 281972; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 6 AGTTGAAGTTG 16
Db 11 AGTTGAGTTG 1
RESULT 27
AB139385/c
ID AB139385 standard; DNA; 12 BP.
XX
AC AB139385;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 339358 for detecting SNP TSC0040959.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PS Claim 1; SEQ ID NO 280261; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 6 AGTTGAAGTTG 16
Db 11 AGTTGAGTTG 1
RESULT 28
ABH80268
ID ABH80268 standard; DNA; 12 BP.
XX
AC ABH80268;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 280261 for detecting SNP TSC0008409.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PS Claim 1; SEQ ID NO 280261; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 47.0%; Score 9.4; DB 5; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 6 AGTTGAAGTTG 16
Db 11 AATTGAGTTG 1
```

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CC  was obtained in electronic format from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences
SQ  Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 12;
  Score over Length 78.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  6 AGTTGAAGTTG 16
Db  ||||| |||
    1 AGTTGAAGTTG 11

RESULT 29
AB114375
ID  AB114375 standard; DNA; 12 BP.
XX  AB114375;
XX  22-FEB-2002 (first entry)
XX  Oligonucleotide primer SEQ ID NO 314348 for detecting SNP TSC0026294.
XX  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX  Homo sapiens.
XX  WO200177384-A2.
XX  18-OCT-2001.
XX  06-APR-2001; 2001WO-IB000713.
XX  07-APR-2000; 2000DE-01019173.
XX  (EPIG-) EPIGENOMICS AG.
XX  Olek A, Piepenbrock C, Berlin K;
XX  WPI; 2001-657177/75.
XX  Set of oligonucleotides, useful for diagnosis and cell typing, is
XX  designed to detect single-nucleotide polymorphisms and cytosine
XX  methylation status.
XX  Claim 1; SEQ ID NO 314348; 29pp + Sequence Listing; German.
XX  This invention describes novel oligonucleotide primers or peptide nucleic
XX  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX  and cytosine methylation status in chemically pretreated genomic DNA. The
XX  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX  range of diseases including immune system, gastrointestinal, respiratory,
XX  central nervous system, cardiovascular and metabolic disorders. The
XX  oligomers are also used for detecting cell type differentiation. ABC00010
XX  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX  represent the oligomers described in the invention. NOTE: The sequence
XX  data for this patent did not form part of the printed specification, but
XX  was obtained in electronic format from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences
XX  Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 12;
  Score over Length 78.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  6 AGTTGAAGTTG 16
Db  ||||| |||||
    1 AGTTGAAGTTG 11

RESULT 31
AEM30648
ID  AEM30648 standard; RNA; 12 BP.
XX  AEM30648;
XX  08-MAR-2007 (first entry)
XX  E. coli rRNA sequence #54.

```

```

Db  2 AGTTAAAGTTG 12

RESULT 30
ABH75142/c
ID  ABH75142 standard; DNA; 12 BP.
XX  ABH75142;
XX  22-FEB-2002 (first entry)
XX  Oligonucleotide primer SEQ ID NO 275133 for detecting SNP TSC0003795.
XX  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX  Homo sapiens.
XX  WO200177384-A2.
XX  18-OCT-2001.
XX  06-APR-2001; 2001WO-IB000713.
XX  07-APR-2000; 2000DE-01019173.
XX  (EPIG-) EPIGENOMICS AG.
XX  Olek A, Piepenbrock C, Berlin K;
XX  WPI; 2001-657177/75.
XX  Set of oligonucleotides, useful for diagnosis and cell typing, is
XX  designed to detect single-nucleotide polymorphisms and cytosine
XX  methylation status.
XX  Claim 1; SEQ ID NO 275133; 29pp + Sequence Listing; German.
XX  This invention describes novel oligonucleotide primers or peptide nucleic
XX  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX  and cytosine methylation status in chemically pretreated genomic DNA. The
XX  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX  range of diseases including immune system, gastrointestinal, respiratory,
XX  central nervous system, cardiovascular and metabolic disorders. The
XX  oligomers are also used for detecting cell type differentiation. ABC00010
XX  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX  represent the oligomers described in the invention. NOTE: The sequence
XX  data for this patent did not form part of the printed specification, but
XX  was obtained in electronic format from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences
XX  Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 12;
  Score over Length 78.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  6 AGTTGAAGTTG 16
Db  ||||| |||||
    12 AGTTGAAGTTG 2

RESULT 31
AEM30648
ID  AEM30648 standard; RNA; 12 BP.
XX  AEM30648;
XX  08-MAR-2007 (first entry)
XX  E. coli rRNA sequence #54.

```

```
XX RNA detection; fluorescence; protein production; bacterial infection;
KW Escherichia coli infection; Pseudomonas aeruginosa infection; ss.
XX Escherichia coli.
XX WO2006122277-A2.
XX 16-NOV-2006.
XX 11-MAY-2006; 2006WO-US018320.
XX 11-MAY-2005; 2005US-0680138P.
XX 25-AUG-2005; 2005US-0711492P.
XX (UYWA-) UNIV WAYNE STATE.
XX Cunningham PR;
XX WPI; 2007-132103/13.
XX
XX New nucleic acids that are conserved and variable regions of Escherichia
PT coli 16S rRNA, useful as targets for pharmaceuticals that are
PT taxonomically specific and/or refractory for developing drug resistance.
XX
XX Example; Fig 5.10; 232pp; English.
XX
XX The invention relates to a nucleic acid represented by a specific
CC formula. The invention also relates to a method of identifying an agent
CC that binds to a nucleic acid, a method of identifying an inhibitor of
CC protein synthesis, a compound obtained by the method and a method of
CC administering a compound to a patient in need. Identifying an agent,
CC which binds to a nucleic acid, thus establishing a first fluorescence
CC reading, contacting a test compound with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a second fluorescence
CC reading, determining the difference between the first fluorescence
CC reading and the second fluorescence reading and selecting the compound
CC where the difference between the first fluorescence reading and the
CC second fluorescence reading is non-zero, thus identifying the agent. It
CC further comprises modifying the agent identified, thus forming a modified
CC agent, contacting the modified agent with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a modified second
CC fluorescence reading, determining the difference between the first
CC fluorescence reading and the modified second fluorescence reading and
CC selecting the compound where the difference between the first
CC fluorescence reading and the second modified fluorescence reading is non-
CC zero, thus identifying a modified agent. Assaying the inhibitory
CC properties of the agent comprises detecting protein synthesis or
CC determining the inhibitor constant for inhibiting mRNA translation. The
CC nucleic acids are conserved and can be used as targets for
CC pharmaceuticals that are taxonomically specific, refractory to the
CC development of drug resistance or both. They can also be used for
CC identifying an inhibitor of protein synthesis. The compound can be
CC administered to a patient having a microbial infection, preferably a
CC bacterial infection, e.g. E. coli or Pseudomonas aeruginosa infection.
XX This sequence represents E. coli rRNA used in the scope of the invention.
XX
XX Sequence 12 BP; 3 A; 1 C; 4 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 47.0%; Score 9.4; DB 22; Length 12;
XX Score over Length 78.3%;
XX Best Local Similarity 63.6%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 6 AGTTGAAGTTG 16
XX ||:||||:|
XX 2 AGUUGAAGCUG 12
XX
XX RESULT 32
XX AEM30671
XX ID AEM30671 standard; RNA; 12 BP.
```

```
XX AEM30671;
XX 08-MAR-2007 (first entry)
XX E. coli rRNA sequence #77.
XX
XX RNA detection; fluorescence; protein production; bacterial infection;
KW Escherichia coli infection; Pseudomonas aeruginosa infection; ss.
XX Escherichia coli.
XX WO2006122277-A2.
XX 16-NOV-2006.
XX 11-MAY-2006; 2006WO-US018320.
XX 11-MAY-2005; 2005US-0680138P.
XX 25-AUG-2005; 2005US-0711492P.
XX (UYWA-) UNIV WAYNE STATE.
XX Cunningham PR;
XX WPI; 2007-132103/13.
XX
XX New nucleic acids that are conserved and variable regions of Escherichia
PT coli 16S rRNA, useful as targets for pharmaceuticals that are
PT taxonomically specific and/or refractory for developing drug resistance.
XX
XX Example; Fig 5.10; 232pp; English.
XX
XX The invention relates to a nucleic acid represented by a specific
CC formula. The invention also relates to a method of identifying an agent
CC that binds to a nucleic acid, a method of identifying an inhibitor of
CC protein synthesis, a compound obtained by the method and a method of
CC administering a compound to a patient in need. Identifying an agent,
CC which binds to a nucleic acid of the invention comprises measuring the
CC fluorescence of the nucleic acid, thus establishing a first fluorescence
CC reading, contacting a test compound with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a second fluorescence
CC reading, determining the difference between the first fluorescence
CC reading and the second fluorescence reading and selecting the compound
CC where the difference between the first fluorescence reading and the
CC second fluorescence reading is non-zero, thus identifying the agent. It
CC further comprises modifying the agent identified, thus forming a modified
CC agent, contacting the modified agent with the nucleic acid and measuring
CC the resulting fluorescence, thus establishing a modified second
CC fluorescence reading, determining the difference between the first
CC fluorescence reading and the modified second fluorescence reading and
CC selecting the compound where the difference between the first
CC fluorescence reading and the second modified fluorescence reading is non-
CC zero, thus identifying a modified agent. Assaying the inhibitory
CC properties of the agent comprises detecting protein synthesis or
CC determining the inhibitor constant for inhibiting mRNA translation. The
CC nucleic acids are conserved and can be used as targets for
CC pharmaceuticals that are taxonomically specific, refractory to the
CC development of drug resistance or both. They can also be used for
CC identifying an inhibitor of protein synthesis. The compound can be
CC administered to a patient having a microbial infection, preferably a
CC bacterial infection, e.g. E. coli or Pseudomonas aeruginosa infection.
XX This sequence represents E. coli rRNA used in the scope of the invention.
XX
XX Sequence 12 BP; 3 A; 1 C; 4 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 47.0%; Score 9.4; DB 22; Length 12;
XX Score over Length 78.3%;
XX Best Local Similarity 63.6%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 6 AGTTGAAGTTG 16
XX ||:||||:|
XX
```

Db 2 AGCUGAAGUUG 12

RESULT 33  
ABV73748/c  
ID ABV73748 standard; DNA; 22 BP.  
XX  
AC ABV73748;  
XX  
DT 30-DEC-2002 (first entry)  
XX  
DE Human Bax sense PCR primer.  
XX  
KW Cell adhesion; apoptosis; peritoneum; Bax; human; vulnery; cytostatic;  
KW antinflammatory; antiinfertility; gene therapy; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200272130-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 11-MAR-2002; 2002WO-US007119.  
XX  
PR 13-MAR-2001; 2001US-0275349P.  
XX  
PA (UYWA-) UNIV WAYNE STATE.  
XX  
PI Diamond MP, Saed GM;  
XX  
DR WPI; 2002-740784/80.  
XX  
PT Preventing or remedying surgical adhesion, useful for preventing  
PT infection, pain or inflammation after surgery or during wound healing, by  
PT modulating apoptosis in peritoneal cells in a subject using Bax agonists  
PT or Bcl-2 antagonists.  
XX  
PS Example 1; Page 16; 24pp; English.  
XX  
CC The present sequence is a sense primer for the human Bax gene coding  
CC region. Use with the antisense primer given in ABV73749 gives a 135 bp  
CC PCR product. Multiplex RT-PCR was used for the simultaneous amplification  
CC of Bcl-2, Bax and beta-actin mRNAs in peritoneal and adhesion fibroblasts  
CC in response to hypoxia. The results showed that adhesion fibroblasts have  
CC almost double the Bcl-2/Bax mRNA ratio as peritoneal fibroblasts. Hypoxia  
CC resulted in a 25% decrease in the Bcl-2/Bax ratio for normal peritoneum  
CC fibroblasts, indicating an increase in apoptosis. Hypoxia also resulted  
CC in a 33% increase in the Bcl-2/Bax ratio for adhesion fibroblasts,  
CC indicating a decrease in apoptosis. The Bcl-2/Bax ratio can determine  
CC whether cells die by apoptosis, or be protected from it. The higher the  
CC ratio, the lower the apoptosis rate. The invention provides a method for  
CC the prevention or remediation of surgical adhesion by modulating  
CC apoptosis in peritoneal, especially fibroblast, cells. The rate of  
CC apoptosis is increased using a therapeutic formulation comprising Bax,  
CC Bax enhancer (e.g. p53), Bax agonist, Bcl-2 inhibitor or Bcl-2  
CC antagonist. A gene therapy method which introduces the p53 or Bax gene  
CC into the fibroblast cells may be used. Determination of the Bcl-2/Bax  
CC ratio can be used to determine whether a human subject, or an organ or  
CC tissue site, is predisposed to develop adhesions during or following  
CC surgery. The method is particularly useful for preventing the development  
CC of post-operative adhesions in of patients following surgery, e.g.  
CC ovarian cystectomy, laparoscopic or open cholecystectomy, colectomy,  
CC splenectomy, kidney transplantation, or caesarean section. It is also  
CC useful in preventing or eliminating cell proliferation or migration,  
CC infection or inflammation during the wound healing process, in preventing  
CC bowel obstruction, pain and infertility, in preventing pannus formation,  
CC or for treating inflammation  
XX  
SQ Sequence 22 BP; 5 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 7; Length 22;  
Score over Length 77.3%;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTGCCTG 20  
|||||  
Db 22 CCAGTTGAAGTGCCTG 6  
|||||

RESULT 34  
AAZ21922/c  
ID AAZ21922 standard; DNA; 13 BP.  
XX  
AC AAZ21922;  
XX  
DT 24-NOV-1999 (first entry)  
XX  
DE Fragment of the VDJ joint of a heterologous antibody.  
XX  
KW Transgenic animal; heterologous antibody; hybridoma; B cell;  
KW transgenic mouse; human heavy chain transgene; digoxin;  
KW human light chain transgene; immortalized cell; immunoglobulin;  
KW Shiga-like toxin; autoimmune disease; cancer; infectious disease;  
KW transplant rejection; blood disorder; coagulation disorder; ss.  
XX  
OS Synthetic.  
XX  
PN WO9945962-A1.  
XX  
PD 16-SEP-1999.  
XX  
PF 12-MAR-1999; 99WO-US005535.  
XX  
PR 13-MAR-1998; 98US-00042353.  
XX  
PA (GENP-) GENPHARM INT INC.  
XX  
PI Lonberg N, Fishwild DM, Ball WJ;  
XX  
DR WPI; 1999-551219/46.  
XX  
PT Novel transgenic non-human animals used to produce heterologous  
PT antibodies.  
XX  
PS Example 12; Page 177; 484pp; English.  
XX  
CC The specification describes transgenic animals that are capable of  
CC producing a heterologous antibody. The antibodies are isolated from a  
CC hybridoma, comprising B cells, that is obtained from a transgenic mouse  
CC having a genome comprising a human heavy chain transgene and a human  
CC light chain transgene. The B cells are fused to immortalized cells  
CC suitable for generating a hybridoma, which produces a detectable amount  
CC of an immunoglobulin that specifically binds digoxin or Shiga-like  
CC toxin. B cells from transgenic animals can be used to generate hybridomas  
CC expressing monoclonal high affinity human sequence antibodies. Antibodies  
CC produced from the transgenic animals of the invention can be used to  
CC treat human diseases, e.g. autoimmune diseases, cancer, infectious  
CC disease, transplant rejection, blood disorders, such as coagulation  
CC disorders and other diseases. AAZ21902-54 represent fragments of the VDJ  
CC joint from 30 clones of the heterologous antibody of the invention  
XX  
SQ Sequence 13 BP; 2 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 2; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 7.3e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTTGA 11  
|||||  
Db 10 CCCAGTTGA 1  
|||||

RESULT 35  
ABF31261/c





PI Olek A, Piepenbrock C, Berlin K;  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 150112; 29pp + Sequence Listing; German.  
PS  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 50.0%; Score 10; DB 5; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 7.3e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 10 AGTTGAAGTT 1  
RESULT 38  
ABF07779/c  
ID ABF07779 standard; DNA; 13 BP.  
XX  
XX ABF07779;  
AC  
XX 21-FEB-2002 (first entry)  
DT  
DE Oligonucleotide SEQ ID NO 107776 for detecting SNP TSC0026982.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 107776; 29pp + Sequence Listing; German.  
PS  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 50.0%; Score 10; DB 5; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 7.3e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 10 AGTTGAAGTT 1  
RESULT 39  
ABC65593/c  
ID ABC65593 standard; DNA; 13 BP.  
XX  
XX ABC65593;  
AC  
XX 21-FEB-2002 (first entry)  
DT  
DE Oligonucleotide SEQ ID NO 65610 for detecting SNP TSC0017271.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 65610; 29pp + Sequence Listing; German.  
PS  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 50.0%; Score 10; DB 5; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 7.3e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 11 AGTTGAAGTT 2



```
Query Match          50.0%; Score 10; DB 5; Length 13;
Score over Length    76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1

RESULT 40
ABF07778
XX ABF07778 standard; DNA; 13 BP.
AC ABF07778;
XX
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 107775 for detecting SNP TSC0026982.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 107775; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match          50.0%; Score 10; DB 5; Length 13;
XX Score over Length    76.9%;
XX Best Local Similarity 100.0%; Pred. No. 7.3e+05;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 AGTTGAAGTT 15
Db 3 AGTTGAAGTT 12

RESULT 41
```

```
ABC28727/c
ID ABC28727 standard; DNA; 13 BP.
XX
XX ABC28727;
AC ABC28727;
XX
XX 20-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 28744 for detecting SNP TSC0008356.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX
XX Claim 1; SEQ ID NO 28744; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match          50.0%; Score 10; DB 5; Length 13;
XX Score over Length    76.9%;
XX Best Local Similarity 100.0%; Pred. No. 7.3e+05;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 AGTTGAAGTT 15
Db 13 AGTTGAAGTT 4

RESULT 42
ABF71655/c
ID ABF71655 standard; DNA; 13 BP.
XX
XX ABF71655;
AC ABF71655;
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 171652 for detecting SNP TSC0042787.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
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XX OS Homo sapiens.
XX PI WO200177384-A2.
XX PN
XX DR
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 171652; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB102073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
    Query Match 50.0%; Score 10; DB 5; Length 13;
    Score over Length 76.9%;
    Best Local Similarity 100.0%; Pred. No. 7.3e+05;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 12 AGTTGAAGTT 3
RESULT 43
ABC28726
ID ABC28726 standard; DNA; 13 BP.
XX AC ABC28726;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 28743 for detecting SNP TSC0008356.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX OS Homo sapiens.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 65609; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB102073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 5 A; 0 C; 3 G; 5 T; 0 U; 0 Other;
    Query Match 50.0%; Score 10; DB 5; Length 13;
    Score over Length 76.9%;
    Best Local Similarity 100.0%; Pred. No. 7.3e+05;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 1 AGTTGAAGTT 10
RESULT 44
ABC65592
ID ABC65592 standard; DNA; 13 BP.
XX AC ABC65592;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 65609 for detecting SNP TSC0017271.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (SPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 65609; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic

```

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 50.0%; Score 10; DB 5; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 7.3e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
Db 4 AGTTGAAGTT 13

RESULT 45  
ABF53415/C  
ID ABF53415 standard; DNA; 13 BP.  
XX  
AC ABF53415;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 153412 for detecting SNP TSC0038780.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
PD 06-APR-2001; 2001WO-IB000713.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 153412; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 13 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 1 Other;  
Query Match 50.0%; Score 10; DB 5; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 83.3%; Pred. No. 7.3e+05;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17  
Db 12 AGTTGAAGATGY 1

RESULT 46  
ABF53414  
ID ABF53414 standard; DNA; 13 BP.  
XX  
AC ABF53414;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 153411 for detecting SNP TSC0038780.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
PD 06-APR-2001; 2001WO-IB000713.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 153411; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 13 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 1 Other;  
Query Match 50.0%; Score 10; DB 5; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 83.3%; Pred. No. 7.3e+05;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17  
Db 2 AGTTGAAGATGY 13

```
RESULT 47
ABF31260
ID ABF31260 standard; DNA; 13 BP.
XX
XX
AC ABF31260;
XX
XX 21-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 131257 for detecting SNP TSC0032754.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 131257; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
SQ
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db 1 GTTGAAGTTG 10
XX
RESULT 48
ABF50114
ID ABF50114 standard; DNA; 13 BP.
XX
XX
AC ABF50114;
XX
XX 21-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 150111 for detecting SNP TSC0037893.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW
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KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 150111; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
SQ
XX Query Match 50.0%; Score 10; DB 5; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 4 AGTTGAAGTT 13
XX
RESULT 49
AEC04526
ID AEC04526 standard; cDNA; 13 BP.
XX
XX AEC04526;
XX
XX 20-OCT-2005 (first entry)
DT
XX
XX Human breast cancer marker cDNA SEQ ID NO 704.
DE
XX
XX Cytostatic; Gene therapy; diagnosis; breast tumor; endocrine disease;
KW gynecology and obstetrics; neoplasm; ss; tumor marker.
XX Homo sapiens.
XX WO2005072050-A2.
XX
XX 11-AUG-2005.
XX
XX 27-JAN-2005; 2005WO-IB000433.
XX
XX 27-JAN-2004; 2004US-0539128P.
XX 27-JAN-2004; 2004US-0539129P.
XX 22-OCT-2004; 2004US-0620656P.
XX
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PR 22-OCT-2004; 2004US-0620853P.
PR 22-OCT-2004; 2004US-0620874P.
PR 22-OCT-2004; 2004US-0620916P.
PR 22-OCT-2004; 2004US-0620917P.
PR 22-OCT-2004; 2004US-0620918P.
PR 22-OCT-2004; 2004US-0620924P.
PR 22-OCT-2004; 2004US-0620974P.
PR 22-OCT-2004; 2004US-0620975P.
PR 22-OCT-2004; 2004US-0621004P.
PR 25-OCT-2004; 2004US-0621131P.
PR 17-NOV-2004; 2004US-00043842.
PR 17-NOV-2004; 2004US-0620123P.
PR 17-NOV-2004; 2004US-0628101P.
PR 17-NOV-2004; 2004US-0628111P.
PR 17-NOV-2004; 2004US-0628112P.
PR 17-NOV-2004; 2004US-0628134P.
PR 17-NOV-2004; 2004US-0628145P.
PR 17-NOV-2004; 2004US-0628156P.
PR 17-NOV-2004; 2004US-0628167P.
PR 17-NOV-2004; 2004US-0628178P.
PR 17-NOV-2004; 2004US-0628231P.
PR 17-NOV-2004; 2004US-0628251P.
PR 27-JAN-2005; 2005US-00043842.
XX
XX (COMP-) COMPUGEN USA INC.
PA Toporik A, Dahary D, Sorek R, Pollock S, Levine Z, Akiva P;
PI Diber A, Novik A, Sella-Tavor O, Ayalon-Soffer M, Walach S;
PI Sameah-Greenwald S, Shemesh R, Keren N, Shklar M;
XX
XX WPI; 2005-555592/56.
XX
XX New human nucleic acid and polypeptide sequences useful for screening,
PT diagnosing or treating breast cancer.
XX
XX Disclosure; SEQ ID NO 704; 1586pp; English.
XX
XX The invention relates to an isolated human polynucleotide. The
CC composition and methods are useful for screening, diagnosing or treating
CC breast cancer. These may also be used in drug screening or in monitoring
CC disease progression and/or treatment efficacy of breast cancer. The
CC present sequence represents a human myoglobin breast cancer marker cDNA.
XX
XX Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 50.0%; Score 10; DB 16; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 7.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db |||||
3 GTTGAAGTTG 12
RESULT 50
AEG12245
ID AEG12245 standard; DNA; 13 BP.
XX
XX AEG12245;
XX
XX 04-MAY-2006 (first entry)
XX
XX Human lung cancer diagnosis related segment T11628_PEA_1_node_32.
XX diagnosis; lung tumor; tumor marker; cytostatic; ds.
XX Homo sapiens.
XX Synthetic.
XX
XX US2006046257-A1.
XX
XX 02-MAR-2006.

```

CC detecting lung cancer cells with the biomarker; (10) selecting a therapy  
CC for lung cancer, which comprises detecting lung cancer cells with the  
CC biomarker and selecting a therapy according to the detection; and (11) a  
CC display library comprising several display vehicles, such as phages,  
CC viruses or bacteria. The isolated polynucleotide is useful in detecting  
CC lung cancer, in monitoring disease progression or treatment efficacy or  
CC relapse of lung cancer or in selecting a therapy for lung cancer. The  
CC invention provides novel markers for lung cancer that are both sensitive  
CC and accurate, something which is not currently provided in the prior art.  
CC The present sequence is used in the exemplification of the present  
CC invention. Note - The Sequence Listing data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from the USPTO web site.

XX  
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 19; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 7.3e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16

DB 3 GTTGAAGTTG 12

RESULT 51

AGI70514  
ID AGI70514 standard; DNA; 13 BP.

XX  
AC AGI70514;

XX  
DT 04-OCT-2007 (first entry)

XX  
DE Human T1628\_PEA\_1\_node\_32 SEQ ID NO: 809.

XX  
KW diagnostic; lung tumor; cancer; neoplasm; cytostatic;  
KW respiratory disease; small-cell lung cancer; non-small cell lung cancer;  
KW adenocarcinoma; squamous cell carcinoma; large cell carcinoma; ds.

XX  
OS Homo sapiens.

XX  
PN WO2006131783-A2.

XX  
PD 14-DEC-2006.

XX  
PF 27-JAN-2005; 2005WO-IB004037.

XX  
PR 27-JAN-2004; 2004US-0539128P.

XX  
PR 27-JAN-2004; 2004US-0539129P.

XX  
PR 22-JUL-2004; 2004US-0589815P.

XX  
PR 07-SEP-2004; 2004US-0607307P.

XX  
PR 22-OCT-2004; 2004US-0620656P.

XX  
PR 22-OCT-2004; 2004US-0620677P.

XX  
PR 22-OCT-2004; 2004US-0620853P.

XX  
PR 22-OCT-2004; 2004US-0620868P.

XX  
PR 22-OCT-2004; 2004US-0620874P.

XX  
PR 22-OCT-2004; 2004US-0620916P.

XX  
PR 22-OCT-2004; 2004US-0620917P.

XX  
PR 22-OCT-2004; 2004US-0620918P.

XX  
PR 22-OCT-2004; 2004US-0620924P.

XX  
PR 22-OCT-2004; 2004US-0620974P.

XX  
PR 22-OCT-2004; 2004US-0620975P.

XX  
PR 22-OCT-2004; 2004US-0621004P.

XX  
PR 25-OCT-2004; 2004US-0621053P.

XX  
PR 25-OCT-2004; 2004US-0621131P.

XX  
PR 17-NOV-2004; 2004US-0628101P.

XX  
PR 17-NOV-2004; 2004US-0628111P.

XX  
PR 17-NOV-2004; 2004US-0628112P.

XX  
PR 17-NOV-2004; 2004US-0628123P.

XX  
PR 17-NOV-2004; 2004US-0628134P.

XX  
PR 17-NOV-2004; 2004US-0628145P.

XX  
PR 17-NOV-2004; 2004US-0628156P.

PR 17-NOV-2004; 2004US-0628167P.

PR 17-NOV-2004; 2004US-0628178P.

PR 17-NOV-2004; 2004US-0628189P.

PR 17-NOV-2004; 2004US-0628251P.

PR 08-DEC-2004; 2004US-0634075P.

PR 27-JAN-2005; 2005US-00051720.

XX  
XX (COMP-) COMPUGEN USA INC.

XX  
XX Pollock S, Levine Z, Novik A, Dahary D, Sorek R, Toporik A;

XX  
XX Sameah-Greenwald S, Sella-Tavor O, Diber A, Cojocaru GS;

XX  
XX Ayalon-Soffer M, Walach S, Akiva P, Keren N, Shmehesh R;

XX  
XX WPI; 2007-159255/16.

XX  
XX New isolated polynucleotide useful as a biomarker for detecting lung

PT cancer comprises polynucleotide having sequence of specified nucleic

PT acids.

XX  
XX Example 5; SEQ ID NO 809; 2200pp; English.

XX  
XX This invention describes novel polynucleotides and polypeptides used for  
CC the diagnosis of lung cancer. The invention claims: a) an antibody  
CC capable of specifically binding to an epitope of an amino acid sequence  
CC of the isolated polypeptide; b) a kit which detects the overexpression of  
CC a splice variant of the isolated polynucleotide; c) a biomarker capable  
CC of detecting lung cancer, comprising a nucleic acid sequence of the  
CC isolated polynucleotide or its fragment, or an amino acid sequence of the  
CC isolated polypeptide or its fragment; d) a method of screening and  
CC diagnosing lung cancer and monitoring disease progression, treatment  
CC efficacy and/or relapse of lung cancer, involving detecting lung cancer  
CC cells with the biomarker and e) selecting a therapy for lung cancer,  
CC involving detecting lung cancer cells with the biomarker and selecting a  
CC therapy according to the detection. The polynucleotides are novel markers  
CC for lung cancer that are both sensitive and accurate and also they are  
CC able to distinguish between different types of lung cancer, such as small  
CC cell or non-small cell lung cancer (e.g. adenocarcinomas, squamous cell  
CC and large cell carcinomas). These markers are overexpressed in lung  
CC cancer specifically, as opposed to normal lung tissue, and thus show a  
CC high degree of differential detection between lung cancer and non-  
CC cancerous states. This sequence represents a polynucleotide used in the  
CC method of the invention.

XX  
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 22; Length 13;

Score over Length 76.9%;

Best Local Similarity 100.0%; Pred. No. 7.3e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16

DB 3 GTTGAAGTTG 12

RESULT 52

ABI38653/C

ID ABI38653 standard; DNA; 12 BP.

XX  
AC ABI38653;

XX  
XX 22-FEB-2002 (first entry)

XX  
DE Oligonucleotide primer SEQ ID NO 338626 for detecting SNP TSC0040587.

XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX  
OS Homo sapiens.

XX  
PN WO200177384-A2.

```

PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 338626; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABIO0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GTTGAAGTT 15
Db 9 GTTGAAGTT 1
|||||

RESULT 53
ABI43950/c
ID ABI43950 standard; DNA; 12 BP.
XX
AC ABI43950;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 343923 for detecting SNP TSC0043299.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 343923 for detecting SNP TSC0043299.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 33923; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABIO0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GTTGAAGTT 15
Db 10 GTTGAAGTT 2
|||||

RESULT 54
ABI33999
ID ABI33999 standard; DNA; 12 BP.
XX
AC ABI33999;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 333972 for detecting SNP TSC0037861.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 333972; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The

```

CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;

Score over Length 75.0%;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16

Db 2 TTGAAGTTG 10

RESULT 55

ABI69281

ID ABI69281 standard; DNA; 12 BP.

XX AC ABI69281;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 369254 for detecting SNP TSC0057554.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 369254; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;

Score over Length 75.0%;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15

Db 4 GTTGAAGTT 12

RESULT 56

ABI42808

ID ABI42808 standard; DNA; 12 BP.

XX AC ABI42808;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 342781 for detecting SNP TSC0042707.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 342781; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;

Score over Length 75.0%;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16

Db 1 TTGAAGTTG 9

RESULT 57

ABH72541

ID ABH72541 standard; DNA; 12 BP.

XX AC ABH72541;



```
XX 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide primer SEQ ID NO 272526 for detecting SNP TSC0002847.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 272526; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 45.0%; Score 9; DB 5; Length 12;
XX Score over Length 75.0%;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 AGTTGAAGT 14
XX
XX DB 4 AGTTGAAGT 12
XX
XX RESULT 58
XX ABH88159
XX ID ABH88159 standard; DNA; 12 BP.
XX
XX AC ABH88159;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 288152 for detecting SNP TSC0013396.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 272526; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 45.0%; Score 9; DB 5; Length 12;
XX Score over Length 75.0%;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 AGTTGAAGT 14
XX
XX DB 4 AGTTGAAGT 12
XX
XX RESULT 58
XX ABH88159
XX ID ABH88159 standard; DNA; 12 BP.
XX
XX AC ABH88159;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 288152 for detecting SNP TSC0013396.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 288152; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
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CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 45.0%; Score 9; DB 5; Length 12;
XX Score over Length 75.0%;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 TTGAAGTTG 16
XX
XX DB 2 TTGAAGTTG 10
XX
XX RESULT 59
XX ABH98609
XX ID ABH98609 standard; DNA; 12 BP.
XX
XX AC ABH98609;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 298602 for detecting SNP TSC0018187.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
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XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
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XX (EPIG-) EPIGENOMICS AG.
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XX Olek A, Piepenbrock C, Berlin K;
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XX WPI; 2001-657177/75.
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XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 288152; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 45.0%; Score 9; DB 5; Length 12;
XX Score over Length 75.0%;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 TTGAAGTTG 16
XX
XX DB 2 TTGAAGTTG 10
XX
XX RESULT 59
XX ABH98609
XX ID ABH98609 standard; DNA; 12 BP.
XX
XX AC ABH98609;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 298602 for detecting SNP TSC0018187.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
```

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 298602; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 TGAAGTTGC 17  
DB 4 TGAAGTTGC 12  
  
RESULT 60  
ABI37700  
ID ABI37700 standard; DNA; 12 BP.  
XX  
AC ABI37700;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 337673 for detecting SNP TSC0039994.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 337673; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;  
  
Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 TTGAAGTTG 16  
DB 2 TTGAAGTTG 10  
  
RESULT 61  
ABI79970  
ID ABI79970 standard; DNA; 12 BP.  
XX  
AC ABI79970;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 379943 for detecting SNP TSC0063547.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 379943; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;  
  
Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;

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Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 4 AGTTGAAGT 12

RESULT 62
ABH98752
ID ABH98752 standard; DNA; 12 BP.
XX AC ABH98752;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 298745 for detecting SNP TSC0018260.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 298745; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15
Db 4 GTTGAAGTT 12

RESULT 63
ABH10039
ID ABH10039 standard; DNA; 12 BP.
XX AC ABH10039;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 319646 for detecting SNP TSC0029341.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 310012; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 2 TTGAAGTTG 10

RESULT 64
ABH19673/c
ID ABH19673 standard; DNA; 12 BP.
XX AC ABH19673;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 319646 for detecting SNP TSC0029341.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 310012; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
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CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
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XX  
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16  
Db 12 TTGAAGTTG 4

RESULT 67  
ABI32591/c  
ID ABI32591 standard; DNA; 12 BP.  
AC ABI32591;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 332564 for detecting SNP TSC0036994.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 332564; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
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CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16  
Db 12 TTGAAGTTG 4

RESULT 69  
ABI45848/c  
ID ABI45848 standard; DNA; 12 BP.  
AC ABI45848;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 284630 for detecting SNP TSC0011911.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 284630; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;

Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16  
Db 12 TTGAAGTTG 4

RESULT 68  
ABH84637/c  
ID ABH84637 standard; DNA; 12 BP.  
XX  
XX  
AC ABH84637;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 284630 for detecting SNP TSC0011911.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 284630; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14  
Db 12 AGTTGAAGT 4

RESULT 69  
ABI45848/c  
ID ABI45848 standard; DNA; 12 BP.  
AC ABI45848;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 284630 for detecting SNP TSC0011911.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 284630; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14  
Db 12 AGTTGAAGT 4

XX	ABI45848;
XX	22-FEB-2002 (first entry)
XX	Olignonucleotide primer SEQ ID NO 345821 for detecting SNP TSC0044228.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
XX	WO200177384-A2.
XX	18-OCT-2001.
XX	06-APR-2001; 2001WO-IB000713.
XX	07-APR-2000; 2000DE-01019173.
XX	(EPIG-) EPIGENOMICS AG.
XX	Olek A, Piepenbrock C, Berlin K;
XX	WPI; 2001-657177/75.
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is
XX	designed to detect single-nucleotide polymorphisms and cytosine
XX	methylation status.
XX	Claim 1; SEQ ID NO 345821; 29pp + Sequence Listing; German.
XX	This invention describes novel oligonucleotide primers or peptide nucleic
XX	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX	and cytosine methylation status in chemically pretreated genomic DNA. The
XX	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX	range of diseases including immune system, gastrointestinal, respiratory,
XX	central nervous system, cardiovascular and metabolic disorders. The
XX	oligoners are also used for detecting cell type differentiation. ABC00010
XX	-ABC99989, ABF0010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX	represent the oligomers described in the invention. NOTE: The sequence
XX	data for this patent did not form part of the printed specification, but
XX	was obtained in electronic format from WIPO at
XX	ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
XX	Query Match 45.0%; Score 9; DB 5; Length 12;
XX	Score over Length 75.0%;
XX	Best Local Similarity 100.0%; Pred. No. 2.2e+06;
XX	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	7 GTTGAAGTT 15
Db	
	9 GTTGAAGTT 1
RESULT 70	
ABI08021	
ID	ABI08021 standard; DNA; 12 BP.
XX	AC ABI08021;
XX	22-FEB-2002 (first entry)
XX	Olignonucleotide primer SEQ ID NO 307994 for detecting SNP TSC0022828.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
XX	OS

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XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 307994; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ASH00010-ASH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GTTGAAGTT 15
DB 4 GTTGAAGTT 12
|||||||
|||||||
RESULT 71
ABI58136
ID ABI58136 standard; DNA; 12 BP.
XX
XX AC ABI58136;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 358109 for detecting SNP TSC0050957.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX
XX

```

XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 358109; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;  
  
Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 TTGAAGTTG 16  
Dd | | | | | | | |  
1 TTGAAGTTG 9  
  
RESULT 72  
ABH99938  
ID ABH99938 standard; DNA; 12 BP.  
XX  
AC ABH99938;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 299931 for detecting SNP TSC0018813.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 299931; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;  
  
Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 TTGAAGTTG 16  
Dd | | | | | | | |  
1 TTGAAGTTG 9  
  
RESULT 73  
AB103368/c  
ID AB103368 standard; DNA; 12 BP.  
XX  
AC AB103368;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 303341 for detecting SNP TSC0020445.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 303341; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;  
  
Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 TTGAAGTTG 16  
Dd | | | | | | | |  
2 TTGAAGTTG 10  
  
RESULT 73  
AB103368/c  
ID AB103368 standard; DNA; 12 BP.  
XX  
AC AB103368;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 303341 for detecting SNP TSC0020445.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 303341; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

```
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14
DB 11 AGTTGAAGT 3

RESULT 74
ABI38557/c
ID ABI38557 standard; DNA; 12 BP.
XX AC
XX AB160242;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 338530 for detecting SNP TSC0005251.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 338530; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
DB 12 TTGAAGTTG 4

RESULT 75
ABI60242/c
ID ABI60242 standard; DNA; 12 BP.
XX AC
XX AB160242;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 360215 for detecting SNP TSC0051979.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 360215; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 5; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14
DB 10 AGTTGAAGT 2

RESULT 76
ABI05053
ID ABI05053 standard; DNA; 12 BP.
XX AC
XX AB105053;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 305026 for detecting SNP TSC0021217.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```



OS Homo sapiens.  
XX WO200177384-A2.  
PN 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB0000713.  
PF 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
PA Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 305026; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 7 GTTGAAGTT 15  
Db 4 GTTGAAGTT 12  
RESULT 77  
ABI69662/c  
ID ABI69662 standard; DNA; 12 BP.  
XX AC ABI69662;  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 369635 for detecting SNP TSC0057764.  
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX WO200177384-A2.  
PN 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB0000713.  
PF 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
PA Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 369635; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 45.0%; Score 9; DB 5; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 7 GTTGAAGTT 15  
Db 4 GTTGAAGTT 12  
RESULT 78  
ABI69662/c  
ID ABI69662 standard; DNA; 12 BP.  
XX AC ABI69662;  
XX 13-AUG-2002 (first entry)  
XX Human OPAL gene, exon/intron junction #13.  
DE Human; ophthalmological; OPAL; autosomal dominant optic atrophy; ADOA;  
KW gene; ds.  
XX OS Homo sapiens.  
XX WO200227022-A2.  
PN 04-APR-2002.  
XX 26-SEP-2001; 2001WO-GB004284.  
PF 26-SEP-2000; 2000GB-00023555.  
XX (UNLO) UNIV COLLEGE LONDON.  
PA (UYEY-) UNIV EYE HOSPITAL.  
XX Bhattacharya S, Wissinger B, Alexander C, Votruba M;  
PI WPI; 2002-416484/44.  
XX Novel human normal or mutant OPAL (the predominant locus for autosomal  
PT dominant optic atrophy (ADOA)) polypeptides and the OPAL gene, useful in  
PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.  
XX Disclosure; Fig 12; 75pp; English.  
XX The invention relates to an isolated human normal or mutant OPAL (the  
CC predominant locus for autosomal dominant optic atrophy (ADOA))

CC polypeptide (I), characterised by a molecular weight of about 112 kDa,  
 CC and substantially free of other human proteins. Also described is the DNA  
 CC (II) encoding (I). (I) and (II) are useful as a medicament, for the  
 CC treatment of a medical condition resulting from a defect in the OPAL  
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid  
 CC and antibodies to (I) are useful in a variety of hybridisation and  
 CC immunological assays to screen for, and to detect the presence of, either  
 CC a normal or a defective OPAL gene or gene product. ABK72533-ABK72593  
 CC represent the human OPAL gene and intron/exon splice junctions

XX Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 45.0%; Score 9; DB 6; Length 12;  
 Score over Length 75.0%;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAG 13  
 |||||  
 Db 4 CAGTTGAAG 12

RESULT 79  
 AAX34784/c  
 ID AAX34784 standard; DNA; 14 BP.

AC AAX34784;  
 XX 02-JUL-1999 (first entry)  
 DT Neurotensin receptor sense PNA oligomer +3765-NTR1-PNA.

XX Polyamide nucleic acid; peptide nucleic acid; PNA; biological response;  
 KW Gene therapy; cancer; aging; behavioral disorder; infection; autoimmune;  
 KW Huntington's disease; Alzheimer's disease; brain disorder; neurotensin;  
 KW ss.

OS Rattus sp.

PN WO9920643-A1.

XX 29-APR-1999.

PF 16-OCT-1998; 98WO-US021888.

PR 17-OCT-1997; 97US-00953269.

PR 30-JAN-1998; 98US-00016685.

PR 08-OCT-1998; 98US-00168519.

PR 08-OCT-1998; 98US-00168714.

PR 08-OCT-1998; 98US-00168791.

XX (MAYO-) MAYO FOUNDATION.

XX Richelson E, Tyler BM, McCormick DJ, Cusack BM, Hoshall CV;

PI Douglas CL, Jansen K;

DR WPI; 1999-302715/25.

XX Extracellular administration of nucleic acid oligomers useful for gene  
 therapy of cancers and behavioral disorders.

PS Claim 14; Page 78; 116pp; English.

XX The invention relates to a method for the treatment of a living cell by  
 CC extracellular administration of a polyamide nucleic acid (PNA) oligomer  
 CC to produce a sequence-specific biological response. A method is also  
 CC provided for identifying mismatch PNA that generate a biological  
 CC response, in an animal, different from that produced by a reference PNA.  
 CC The PNA oligomers are used to manipulate and study any polypeptide in  
 CC living cells, either for research (e.g. identifying polypeptide functions  
 CC or measuring the relative turn-over rate of functional polypeptides) or  
 CC for gene therapy of e.g. cancer, aging, behavioral disorders, infections  
 CC and autoimmune diseases, typically Huntington's and Alzheimer's diseases.

CC They can cross biological barriers (making them suitable for treating  
 CC brain disorders) and elicit a sequence-specific response, eliminating the  
 CC need for microinjection into cells or for cell permeabilization. They may  
 CC modulate polypeptide expression by both sense and antisense mechanisms  
 CC (which may be used together), and using PNA with controllable degrees of  
 CC mismatch allows the response to be adjusted as required

XX Sequence 14 BP; 4 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

QY Query Match 52.0%; Score 10.4; DB 2; Length 14;  
 Score over Length 74.3%;  
 Best Local Similarity 91.7%; Pred. No. 4.7e+05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16  
 |||||  
 Db 14 CAGATGAAGTTG 3

RESULT 80

ABC61646

ID ABC61646 standard; DNA; 13 BP.

XX ABC61646;

XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 61663 for detecting SNP TSC0016401.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

PN 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 61663; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 1 Other;

QY Query Match 48.0%; Score 9.6; DB 5; Length 13;  
 Score over Length 73.8%;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+06;

```

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TTGAAGTTGC 17
Db 4 TTGAAGTTGY 13
RESULT 81
ABC61647/c
ID ABC61647 standard; DNA; 13 BP.
XX
AC ABC61647;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 61664 for detecting SNP TSC0016401.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 61664; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABF9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABT0010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 1 Other;

Query Match 48.0%; Score 9.6; DB 5; Length 13;
Score over Length 73.8%;
Best Local Similarity 90.0%; Pred. No. 1.1e+06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGC 17
Db 10 TTGAAGTTGY 1
RESULT 82
AAx75746/c
ID AAx75746 standard; RNA; 15 BP.
XX
XX AAx75746;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt-1 and KDR hammerhead ribozyme target site #80.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Example 9; Page 192; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX6725 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
SQ Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 55.0%; Score 11; DB 2; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14
Db 15 CCAGTTGAAGT 5
RESULT 83
AAZ64449/c
ID AAZ64449 standard; RNA; 15 BP.
XX
XX AAZ64449;
XX
XX 28-MAR-2000 (first entry)
XX
XX Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 9176.
XX
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
XX cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX autoimmune disease; ss.
XX
XX Hepatitis C virus.

```

XX PN WO9955847-A2.  
XX PD 04-NOV-1999.  
XX PP 26-APR-1999; 99WO-US009027.  
XX PR 27-APR-1998; 98US-0083217P.  
XX PR 18-SEP-1998; 98US-0100842P.  
XX PR 25-FEB-1999; 99US-00257608.  
XX PR 23-MAR-1999; 99US-00274553.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;  
XX DR WPI; 2000-062023/05.  
XX PT Novel ribozymes for the treatment of diseases and conditions related to  
XX PT hepatitis C infection.  
XX PS Claim 1; Page 92; 123pp; English.  
XX SS The present sequence represents the preferred target sequence of an  
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in  
CC the descriptor line. The HCV sequence was screened for optimal ribozyme  
CC target sites using a computer folding algorithm and regions of the mRNA  
CC which did not form secondary folding structures and contained potential  
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to  
CC target these sites and their activities optimised by either varying the  
CC length of the binding arms or by modification to prevent degradation by  
CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
CC viral replication, and are used to treat diseases associated with  
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
CC hepatocellular carcinoma. The ribozymes may be used in combination with  
CC interferon to treat HCV infection, other infectious diseases, autoimmune  
CC diseases, and cancer  
XX SQ Sequence 15 BP; 3 A; 5 C; 3 G; 0 T; 4 U; 0 Other;  
Query Match 55.0%; Score 11; DB 3; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 CCCAGTTGAAG 13  
Db 15 CCCAGTTGAAG 5  
RESULT 84  
ID AEB76210/c  
XX AEB76210 standard; RNA; 15 BP.  
XX AC AEB76210;  
XX DT 22-SEP-2005 (first entry)  
XX DE Hepatitis C virus hammerhead ribozyme substrate sequence.  
KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;  
KW antiviral; gene therapy; substrate; ss.  
XX OS Hepatitis C virus.  
XX PN US2002013458-A1.  
XX PD 31-JAN-2002.  
XX PF 15-FEB-2000; 2000US-00504231.  
XX PR 23-MAR-1999; 99US-00274553.

XX PA (BLAT/) BLATT L.  
XX PA (NCSW/) MCSWIGGEN J A.  
XX PA (ROBE/) ROBERTS E.  
XX PA (PAVO/) PAVO P A.  
XX PA (MACE/) MACEJACK D.  
XX PI Blatt L, McSwiggen JA, Roberts E, Pavo PA, Macejack D;  
XX DR WPI; 2002-215899/27.  
XX PT New enzymatic nucleic acid molecule, which specifically cleaves minus  
XX PT strand RNA derived from hepatitis C virus, useful for modulating the  
XX PT expression and/or replication of hepatitis C virus.  
XX PS Example 1; Page 42; 65pp; English.  
XX SS The invention relates to an enzymatic nucleic acid molecule which  
CC specifically cleaves minus strand RNA derived from hepatitis C virus  
CC (HCV). The binding arms of the molecule comprise ribozyme sequences. The  
CC molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and  
CC Zinzyne motifs. Also described: (1) a pharmaceutical composition  
CC comprising the novel enzymatic nucleic acid; (2) a mammalian cell  
CC including the novel enzymatic nucleic acid; (3) an expression vector  
CC comprising a nucleic acid sequence encoding at least one enzymatic  
CC nucleic acid molecule, in a manner, which allows expression of that  
CC molecule; (4) a mammalian cell including an expression vector of (3); (5)  
CC methods for treating cirrhosis, liver failure or hepatocellular carcinoma  
CC by administering to a patient the novel enzymatic nucleic acid or the  
CC vector of (3); (6) a method of treating a patient having a condition  
CC associated with HCV infection, by contacting cells of the patient with  
CC the nucleic acid molecule, and further employing one or more drug  
CC therapies; (7) a method for inhibiting HCV replication in a mammalian  
CC cell by administering the novel enzymatic nucleic acid; and (8) a method  
CC of cleaving a separate RNA molecule by contacting the novel enzymatic  
CC nucleic acid with the separate RNA molecule. The enzymatic nucleic acid  
CC is useful for modulating the expression and/or replication of hepatitis C  
CC virus (HCV), and for inhibiting the expression of HCV minus strand. The  
CC nucleic acid may also be used to treat or prevent the occurrence of a  
CC disease state in a patient. The present sequence represents an HCV  
CC hammerhead ribozyme target substrate sequence which is used in the  
CC exemplification of the present invention.  
XX SQ Sequence 15 BP; 3 A; 5 C; 3 G; 0 T; 4 U; 0 Other;  
Query Match 55.0%; Score 11; DB 6; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 CCCAGTTGAAG 13  
Db 15 CCCAGTTGAAG 5  
RESULT 85  
ID AEBX01502/c  
XX AEBX01502 standard; RNA; 15 BP.  
XX AC AEBX01502;  
XX DT 23-DEC-2002 (first entry)  
XX DE Hepatitis C virus substrate #1284 for HCV hammerhead ribozyme #1284.  
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
KW type I interferon; interferon alpha; interferon beta; cytostatic;  
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
KW substrate; hammerhead ribozyme; HH ribozyme; ss.  
XX OS Hepatitis C virus.

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XX PN US2002082225-A1.
XX PD . 27-JUN-2002.
XX PF 23-MAR-1999; 99US-00274553.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS B.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX PR WPI; 2002-617759/66.
XX DR
XX CC New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX CC replication and are useful to treat hepatitis C virus infections and
XX CC cirrhosis, liver failure or hepatocellular carcinoma.
XX PS Claim 1; Page 58; 80pp; English.
XX CC The present invention relates to enzymatic nucleic acids which
XX CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX CC (HP) motif where the binding arms comprise sequences complementary to one
XX CC of the substrate sequences defined in the specification. The HCV
XX CC ribozymes are useful for modulating the expression and/or replication of
XX CC HCV. They can be used to treat cirrhosis, liver failure and/or
XX CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX CC a condition associated with HCV infection in conjunction with one or more
XX CC other drug therapies, particularly type I interferon, especially
XX CC interferon alpha, beta or gamma or consensus interferon. The present
XX CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
XX CC Some of the sequence data for this patent did not form part of the
XX CC printed specification. The complete sequence data for this patent was
XX CC obtained in electronic format directly from the USPTO web site at
XX CC seqdata.uspto.gov/psipdsIDEntry.html
XX SQ Sequence 15 BP; 3 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 55.0%; Score 11; DB 6; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 86
ABQ77353/c
ID ABQ77353 standard; DNA; 15 BP.
XX AC ABQ77353;
XX DT 08-MAY-2003 (first entry)
XX DE Receptor synthesis associated oligonucleotide probe #4.
XX KW Probe; wet chemical; photochemical; receptor synthesis; immobilisation;
XX KW polymetric receptor; array; nucleic acid chip; computer-optimisation; ss.
XX OS Synthetic.
XX PN DE10122357-A1.
XX PD 14-NOV-2002.
XX

09-MAY-2001; 2001DE-01022357.
09-MAY-2001; 2001DE-01022357.
(FEBI-) FEBIT FERRARIUS BIOTECHNOLOGY GMBH.
Staehler CF, Staehler PF, Beier M, Wixmerten A, Mauritz R;
Schlausersbach A;
WPI; 2003-240759/24.
Preparation of carrier for determining analytes, useful particularly for
making DNA chips, uses both wet chemical and photochemical techniques for
receptor synthesis.
Disclosure; Fig 11; 24pp; German.
This invention describes a novel method for the preparation of a carrier
for determination of analytes using a combination of wet chemical and
photochemical techniques for synthesis of receptors. The method comprises
(i) passing a liquid containing nucleic acid building blocks for
synthesis of a polymetric receptor over a carrier, (ii) location- and/or
time-specific immobilisation of the building blocks at predetermined
regions and (iii) repeating the procedure to synthesise the required
polymetric receptor at selected positions. The novel feature is that
polymetric repeats are synthesised using a combination of wet chemical and
photochemical stages. The carrier described in the invention is a
receptor array, particularly a nucleic acid chip (but also arrays of
proteins, peptides and saccharides), e.g. for genomic, gene expression or
chemical and photochemical techniques, allowing preparation of many
different receptors at the same site (not possible with either technique
alone). It also allows computer-optimisation of the synthesis strategy,
including use of as many wet-chemical steps as possible for optimal
quality and greater synthesis rate. ABQ77350-ABQ77354 represent
oligonucleotide probes used to illustrate the method of the invention
Sequence 15 BP; 5 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 8; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCC 18
Db 14 TTGAAGTTGCC 4

RESULT 87
AAQ88636
ID AAQ88636 standard; DNA; 12 BP.
XX AC AAQ88636;
XX DT 03-JAN-1996 (first entry)
XX DE Human mitochondrial D-loop region DNA probe 16-12.
XX KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
XX KW D-loop region; biological chip; hybridisation fingerprint;
XX KW interrogation position; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 12
XX FT /*tag= a
XX FT /note= "3'-end of probe is covalently attached to chip
XX PN W09511995-A1.
XX

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PD 04-MAY-1995.
XX
XX PF 26-OCT-1994; 94WO-US012305.
XX
XX PR 26-OCT-1993; 93US-00143312.
XX
XX PR 02-AUG-1994; 94US-00284064.
XX
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
XX PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
XX PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX
XX DR WPI; 1995-178887/23.
XX
XX PT New arrays of oligo:nucleotide probes - used for comparing known
XX PT sequences with variants for detection of mutation(s) and sequencing.
XX
XX PS Disclosure; Page 108; 223pp; English.
XX
XX CC A DNA chip was prepared for analysing sequences contained in a 1.3kb
XX CC fragment of human mitochondrial DNA from the D-loop region, the most
XX CC polymorphic region of human mitochondrial DNA. The chip comprised a set
XX CC of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
XX CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
XX CC x 1cm array. Each position in the sequence was represented by at least
XX CC one probe (usually 2 or more). DNA was amplified from six human donors
XX CC and then transcribed to give the 1.3kb RNA transcripts which were
XX CC fragmented and hybridised to the chip. For each individual, a unique
XX CC hybridisation fingerprint was produced on the chip; all differences could
XX CC be correlated with differences in the cloned genomic DNA sequence
XX
XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
DB 1 ATTTGGAGTTGC 12

RESULT 88
AAQ88635
ID AAQ88635 standard; DNA; 12 BP.
XX
XX AC AAQ88635;
XX
XX DT 03-JAN-1996 (first entry)
XX
XX DE Human mitochondrial D-loop region DNA probe 15-12.
XX
XX KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
XX KW D-loop region; biological chip; hybridisation fingerprint;
XX KW interrogation position; ss.
XX
XX OS Synthetic.
XX
XX FH Key
XX modified_base 12
XX /tag= a
XX /notes="3'-end of probe is covalently attached to chip
XX surface"
XX
XX PN W09511995-A1.
XX
XX PD 04-MAY-1995.
XX
XX PF 26-OCT-1994; 94WO-US012305.
XX
XX PR 26-OCT-1993; 93US-00143312.
XX
XX PR 02-AUG-1994; 94US-00284064.
XX
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
XX PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
XX PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX
XX DR WPI; 1995-178887/23.
XX
XX PT New arrays of oligo:nucleotide probes - used for comparing known
XX PT sequences with variants for detection of mutation(s) and sequencing.
XX
XX PS Disclosure; Page 108; 223pp; English.
XX
XX CC A DNA chip was prepared for analysing sequences contained in a 1.3kb
XX CC fragment of human mitochondrial DNA from the D-loop region, the most
XX CC polymorphic region of human mitochondrial DNA. The chip comprised a set
XX CC of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
XX CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
XX CC x 1cm array. Each position in the sequence was represented by at least
XX CC one probe (usually 2 or more). DNA was amplified from six human donors
XX CC and then transcribed to give the 1.3kb RNA transcripts which were
XX CC fragmented and hybridised to the chip. For each individual, a unique
XX CC hybridisation fingerprint was produced on the chip; all differences could
XX CC be correlated with differences in the cloned genomic DNA sequence
XX
XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 2; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 1 TGGAGTTGCAGT 12

RESULT 89
AAZ30061
ID AAZ30061 standard; DNA; 12 BP.
XX
XX AC AAZ30061;
XX
XX DT 26-JAN-2000 (first entry)
XX
XX DE Splice acceptor site of exon 3 of IL-1 receptor antagonist DNA.
XX
XX KW Human; interleukin-1 receptor; IL-1; antagonist; sepsis;
XX KW acute pancreatitis; endotoxin shock; cytokine induced shock;
XX KW rheumatoid arthritis; chronic inflammatory arthritis;
XX KW pancreatic cell damage; diabetes mellitus type 1;
XX KW graft versus host disease; inflammatory bowel disease; inflammation;
XX KW pulmonary disease; autoimmune disease; inflammatory disease;
XX KW antiproliferative; myelogenous leukemia; premature labor;
XX KW intrauterine infection; nutritional activity;
XX KW hematopoiesis regulating activity; tissue growth activity;
XX KW activin activity; inhibit activity; chemotactic activity;
XX KW chemokinetic activity; hemostatic activity; thrombolytic activity;
XX KW anti-inflammatory activity; splice donor site; ss.
XX
XX OS Homo sapiens.
XX
XX PN W09951744-A2.
XX
XX PD 14-OCT-1999.
XX
XX PF 05-APR-1999; 99WO-US004291.
XX
XX PR 03-APR-1998; 98US-00055010.
XX
XX PR 15-MAY-1998; 98US-00079909.
XX
XX PR 20-MAY-1998; 98US-00082364.
XX
XX PR 19-JUN-1998; 98US-00099818.
XX
XX PR 31-JUL-1998; 98US-00127698.

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PR 13-JAN-1999; 99US-00229591.
PR 17-FEB-1999; 99US-00251370.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Ford J, Pace A, Alfienito M;
XX
DR WPI; 1999-611042/52.
XX
PT New isolated interleukin-1 receptor binding polypeptides, used to treat
PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,
PT inflammatory disease, autoimmune disease or proliferative disease.
XX
PS Example 8; Page 94; 123pp; English.
XX
CC AA230056-63 represent splice donor and splice acceptor sites of a genomic
CC clone encoding IL-1 receptor antagonist. The receptor antagonist
CC polynucleotides and polypeptides can be used for the prevention or
CC treatment of disorders involving sepsis, acute pancreatitis, endotoxemic
CC shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory
CC arthritis, pancreatic cell damage from diabetes mellitus type 1, graft
CC versus host disease, inflammatory bowel disease, inflammation associated
CC with pulmonary disease, other autoimmune disease or inflammatory disease,
CC an antiproliferative agent such as for acute or chronic myelogenous
CC leukemia or in the prevention of premature labor secondary to
CC intrauterine infections. They can also exhibit activities such as e.g.
CC nutritional activity, cytokine and cell proliferation/ differentiation
CC activity, immune stimulating or suppressing activity, hematopoiesis
CC regulating activity, tissue growth activity, activin/ inhibin activity,
CC chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,
CC receptor/ ligand activity, and anti-inflammatory activity. The products
CC can also be used for detection, diagnosis and drug screening
XX
SQ Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
    Query Match 44.0%; Score 8.8; DB 2; Length 12;
    Score over Length 73.3%;
    Best Local Similarity 83.3%; Pred. No. 2.8e+06;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAG 13
Db 1 CCACAGGTGAAG 12

RESULT 90
AAAF31364
ID AA31364 standard; DNA; 12 BP.
AC
AC AA31364;
XX
DT 05-APR-2001 (first entry)
XX
DE Intron/exon junction sequence #5.
XX
KW interleukin; IL-1 receptor; cancer; inflammation; ds.
XX
OS Unidentified.
XX
XX WO200102571-A2.
XX
XX 11-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US018710.
XX
PR 07-JUL-1999; 99US-00348942.
PR 13-OCT-1999; 99US-00417455.
PR 08-DEC-1999; 99US-00457626.
PR 10-MAR-2000; 2000US-00523552.
PR 22-MAY-2000; 2000US-00576008.
XX
PA (HYSE-) HYSEQ INC.
XX
Ford J, Pace A;
WPI; 2001-071582/08.
Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist
proteins (referred as IL-1Hv1), useful in the treatment of cancer, e.g.
breast adenocarcinoma and brain tumors, and an inflammatory disease
mediated by IL-18.
Example 8; Page 123; 179pp; English.
The present invention relates to interleukin (IL)-1 receptor antagonist
proteins. IL-1Hv1 is useful for treating cancer, an inflammatory disease
mediated by IL-18, inflammation resulting from infection or allergic
reactions, and inflammation associated with chronic bronchitis,
arthritis, diabetes or endothermia
Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
    Query Match 44.0%; Score 8.8; DB 4; Length 12;
    Score over Length 73.3%;
    Best Local Similarity 83.3%; Pred. No. 2.8e+06;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAG 13
Db 1 CCACAGGTGAAG 12

RESULT 91
AAAF31364
ID AA31364 standard; DNA; 12 BP.
AC
AC AA31364;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human pregnane X receptor (hPXR) gene, PCR primer #32.
XX
KW Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
KW therapeutic; chemotherapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
XX WO200120026-A2.
XX
XX 22-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-EF008827.
XX
XX 10-SEP-1999; 99EP-00118120.
XX
XX (EPID-) EPIDAUFROS BIOTECHNOLOGIE AG.
XX
XX Wojnowski L, Hustert E;
XX
XX WPI; 2001-273428/28.
XX
XX Novel variant of the human pregnane X receptor gene, associated with
XX insufficient metabolism and/or sensitivity to drugs, is useful for
XX diagnosing and treating diseases with drugs that are modulators of their
XX gene product.
XX
XX Claim 37; Page 39; 108pp; English.
XX
XX AA302731-AA302909 represent human pregnane X receptor (hPXR) coding
XX sequences and PCR primers of the invention. The human pregnane X receptor
XX sequences are used to make antibodies, or a substance capable of binding
XX specifically to the gene product of hPXR gene, for diagnosing and
XX treating various diseases, such as cancer, with drugs that are
XX substrates, inhibitors or modulators of the hPXR gene product. The
XX proteins can be used to identify and obtain prodrugs and drugs for

```

CC treatment of diseases which are amenable to chemotherapy. The nucleic  
CC acids can be used in gene therapy for the treatment or prevention of  
CC disorders associated with hpxr expression

XX Sequence 12 BP; 2 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 4; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 2.8e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAGG 13

|||||

1 CCCAGGTGAGG 12

RESULT 92

ABI22912

ID ABI22912 standard; DNA; 12 BP.

XX

AC ABI22912;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 322885 for detecting SNP TSC0031095.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

OS

XX WO200177384-A2.

PN

XX 18-OCT-2001.

PD

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIC-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

XX WPI; 2001-657177/75.

DR

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX

PS Claim 1; SEQ ID NO 322885; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 5; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 2.8e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAGTTGTC 17

|||||

1 AGTTGAGGTGTC 12

Db 1 AGTTGAGGTGTC 12

RESULT 93

ABI69899

ID ABI69899 standard; DNA; 12 BP.

XX

AC ABI69899;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 369872 for detecting SNP TSC0057857.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

OS

XX WO200177384-A2.

PN

XX 18-OCT-2001.

PD

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIC-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

XX WPI; 2001-657177/75.

DR

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX

PS Claim 1; SEQ ID NO 369872; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 5; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 2.8e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAGTTGTC 17

|||||

1 AGTTGAGGTGTC 12

RESULT 94

ABI23159/C

ID ABI23159 standard; DNA; 12 BP.

XX

AC ABI23159;

XX

DT 22-FEB-2002 (first entry)

XX



DE Oligonucleotide primer SEQ ID NO 323132 for detecting SNP TSC0031232.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 323132; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 2 A; 5 C; 2 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCGCGAGTTGAA 12  
Db 12 GCGCGAGTTGAA 1  
RESULT 95  
ABI53494  
ID ABI53494 standard; DNA; 12 BP.  
XX  
XX ABI53494;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide primer SEQ ID NO 353467 for detecting SNP TSC0048527.  
DE  
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX

PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 353467; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 9 TCAAGTTGCCGT 20  
Db 1 TGAAGTGGACGT 12  
RESULT 96  
ABI73838  
ID ABI73838 standard; DNA; 12 BP.  
XX  
XX ABI73838;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide primer SEQ ID NO 373811 for detecting SNP TSC0060333.  
DE  
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT

PT methylation status.  
PS Claim 1; SEQ ID NO 373811; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;  
Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTGC 17  
DB 1 AGTTGATTTTC 12  
RESULT 97  
ABH75115/c  
ID ABH75115 standard; DNA; 12 BP.  
XX  
XX ABH75115;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 275104 for detecting SNP TSC0003785.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 275104; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;  
Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTGC 17  
DB 1 AGTTGATTTTC 12  
RESULT 97  
ABH75115/c  
ID ABH75115 standard; DNA; 12 BP.  
XX  
XX ABH75115;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 275104 for detecting SNP TSC0003785.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 275104; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;  
Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCCCCAGTTGAA 12  
DB 12 GCCCCACTTTAA 1  
RESULT 98  
ABH90898  
ID ABH90898 standard; DNA; 12 BP.  
XX  
XX ABH90898;  
XX  
XX 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 290891 for detecting SNP TSC0014559.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 290891; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 6 AGTTGAAGTTCG 17
DB 1 AGTTGATGTAGC 12

RESULT 99
ABI26910
ID ABI26910 standard; DNA; 12 BP.
XX ABI26910;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 326883 for detecting SNP TSC0033322.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 317181; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 1 A; 1 C; 5 G; 5 T; 0 U; 0 Other;
XX Query Match 44.0%; Score 8.8; DB 5; Length 12;
XX Score over Length 73.3%;
XX Best Local Similarity 83.3%; Pred. No. 2.8e+06;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 1 TGAGGTTCGT 12

RESULT 100
ABI17208/c
ID ABI17208 standard; DNA; 12 BP.
XX ABI17208;
XX 22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 317181 for detecting SNP TSC0027856.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 317181; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 44.0%; Score 8.8; DB 5; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19
DB 12 TTGAGTTGCCG 1

RESULT 101
ABI27176/c
ID ABI27176 standard; DNA; 12 BP.
XX ABI27176;
XX 22-FEB-2002 (first entry)
Oligonucleotide primer SEQ ID NO 327149 for detecting SNP TSC0033464.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.

```

XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIC-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 327149; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;  
 XX  
 XX Query Match 44.0%; Score 8.8; DB 5; Length 12;  
 XX Score over Length 73.3%;  
 XX Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
 XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX QY 9 TGAAGTTGCCGT 20  
 XX |||||  
 XX 12 TGAAGTTGTGGT 1  
 XX  
 XX  
 XX RESULT 102  
 XX ABI44809  
 XX ID ABI44809 standard; DNA; 12 BP.  
 XX  
 XX AC ABI44809;  
 XX  
 XX DT 22-FEB-2002 (first entry)  
 XX  
 XX DE Oligonucleotide primer SEQ ID NO 344782 for detecting SNP TSC0043703.  
 XX  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN WO200177384-A2.  
 XX  
 XX PD 18-OCT-2001.  
 XX  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX  
 XX PA (EPIC-) EPIGENOMICS AG.  
 XX  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX DR WPI; 2001-657177/75.  
 XX  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 344782; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
 XX  
 XX Query Match 44.0%; Score 8.8; DB 5; Length 12;  
 XX Score over Length 73.3%;  
 XX Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
 XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX QY 6 AGTTGAAGTTGC 17  
 XX |||||  
 XX 1 AGTTGAGATTGC 12  
 XX  
 XX  
 XX RESULT 103  
 XX ABI58076/c  
 XX ID ABI58076 standard; DNA; 12 BP.  
 XX  
 XX AC ABI58076;  
 XX  
 XX DT 22-FEB-2002 (first entry)  
 XX  
 XX DE Oligonucleotide primer SEQ ID NO 358049 for detecting SNP TSC0050929.  
 XX  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN WO200177384-A2.  
 XX  
 XX PD 18-OCT-2001.  
 XX  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX  
 XX PA (EPIC-) EPIGENOMICS AG.  
 XX  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX DR WPI; 2001-657177/75.  
 XX  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 358049; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 5; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTCCGT 20  
Db 12 TGAAGTTGGAGT 1

RESULT 104

AAD52648  
ID AAD52648 standard; DNA; 12 BP.

XX AC AAD52648;

XX DT 14-MAY-2003 (first entry)

XX DE Human ALT2 gene intron3/exon4 junction DNA.

XX KW Human; alanine transaminase; ALT2; diagnosis; injury; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX FT intron 1..6

XX FT /tag= a

XX FT /number= 3

XX FT /partial

XX FT 11..12

XX FT /tag= b

XX FT /number= 4

XX FT /partial

XX PN WO200292768-A2.

XX PD 21-NOV-2002.

XX PF 14-MAY-2002; 2002WO-US015103.

XX PR 14-MAY-2001; 2001US-0290829P.

XX PA (UYMA-) UNIV MARYLAND BALTIMORE.

XX PI Gong D, Shuldiner A, Yang R;

XX DR WPI; 2003-129280/12.

XX PT New human alanine transaminase polypeptide (ALT2) and gene, useful for  
XX detecting injury, damage or disease involving a tissue that contains the  
XX ALT2 in an animal, or in diagnosing conditions associated with altered  
XX levels of ALT2.

XX PS Disclosure; Page 14; 57pp; English.

XX CC The invention relates to human alanine transaminase polypeptide (ALT2)  
XX and gene. The invention is useful for diagnosing or detecting injury,  
XX damage or disease involving a tissue that contains the ALT2 polypeptide  
XX in an animal, in diagnosing conditions associated with altered levels of  
XX ALT2 and/or ALT1 in bodily fluids. The present sequence is human ALT2  
XX gene intron/exon junction DNA

XX SQ Sequence 12 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 8; Length 12;

Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13  
Db 1 CCCAGGTGATG 12

RESULT 105

AEC62435/c  
ID AEC62435 standard; DNA; 12 BP.

XX AC AEC62435;

XX DT 17-NOV-2005 (first entry)

XX DE Human gene fragment VH1-18 mutant SEQ ID NO 45.

XX KW DNA sequencing; DNA amplification; DNA microarray; VH1-18; ds; mutant.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2005084134-A2.

XX PD 15-SEP-2005.

XX PF 06-MAR-2005; 2005WO-IL000263.

XX PR 04-MAR-2004; 2004US-0549541P.

XX PA (LESH/) LESHKOWITZ D.

XX PI Leshkowitz D;

XX DR WPI; 2005-639011/65.

XX PT Sequencing population of polynucleotide (PP) by forming hybridization  
XX duplex of known oligonucleotide and PP, detecting oligonucleotide  
XX involved in duplex formation and compiling set of sequences of PP.

XX PS Example 1; SEQ ID NO 45; 102pp; English.

XX CC The invention describes a method of sequencing (M1) a population of  
XX polynucleotides encoding antibodies or T-cell receptors, comprising  
XX contacting oligonucleotides of known sequences with population of  
XX polynucleotides, to allow formation of hybridization duplexes,  
XX quantitatively detecting oligonucleotides involved in formation of the  
XX hybridization duplexes and compiling set of sequences of the population  
XX of polynucleotides. Also described are: quantifying an expression of a  
XX population of polynucleotides encoding antibodies or T-cell receptors,  
XX comprising carrying out the steps of (M1), and determining a level of  
XX each set of the compiled set of sequences of assembling step in the  
XX population of polynucleotides, therefore quantifying the expression of  
XX the population of polynucleotides encoding the antibodies or T-cell  
XX receptors; and an oligonucleotide library (I) for sequencing by  
XX hybridization of polynucleotides encoding variable regions of antibodies  
XX or T cell receptors, comprising essentially of a set of overlapping  
XX oligonucleotides collectively selected to hybridize with all germline  
XX segments encoding the variable regions of the antibodies or T cell  
XX receptors under conditions allowing formation of hybridization duplexes  
XX between the set of overlapping oligonucleotides and the polynucleotides,  
XX and variant set of oligonucleotides of the overlapping oligonucleotides,  
XX which comprises (C, T, A) base variation in one or more positions of  
XX the overlapping oligonucleotides. (M1) is useful for sequencing a  
XX population of polynucleotides encoding antibodies or T-cell receptor.  
XX (M1) enables a high-throughput method of sequencing a population of  
XX polynucleotides that is having the ability to screen a broad spectrum of  
XX samples, and allows the analysis of a large amount of cells and samples  
XX in a fast manner in order to identify a number of relevant target nucleic  
XX acids. This sequence represents a mutated human gene fragment VH1-18  
XX associated with the sequencing method of the invention.

XX SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 44.0%; Score 8.8; DB 17; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16  
||| ||||| |||  
DB 12 CAGTTGAAGTTG 1

RESULT 106  
ID AEC62417/c  
XX AEC62417 standard; DNA; 12 BP.  
XX AC AEC62417;  
XX DT 17-NOV-2005 (first entry)  
XX DE Human gene fragment VH1-18 mutant SEQ ID NO 27.  
XX KW DNA sequencing; DNA amplification; DNA microarray; VH1-18; ds; mutant.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO2005084134-A2.  
XX PD 15-SEP-2005.  
XX PF 06-MAR-2005; 2005WO-IL000263.  
XX PR 04-MAR-2004; 2004US-0549541P.  
XX PA (LESH/) LESHKOWITZ D.  
XX PI Leshkowitz D;  
XX DR WPI; 2005-639011/65.  
XX PS Sequencing population of polynucleotide (PP) by forming hybridization duplex of known oligonucleotide and PP, detecting oligonucleotide involved in duplex formation and compiling set of sequences of PP.  
XX Example 1; SEQ ID NO 27; 102pp; English.  
XX The invention describes a method of sequencing (M1) a population of polynucleotides encoding antibodies or T-cell receptors, comprising contacting oligonucleotides of known sequences with population of polynucleotides, to allow formation of hybridization duplexes, quantitatively detecting oligonucleotides involved in formation of the hybridization duplexes and compiling set of sequences of the population of polynucleotides. Also described are: quantifying an expression of a population of polynucleotides encoding antibodies or T-cell receptors, comprising carrying out the steps of (M1), and determining a level of each set of the compiled set of sequences of assembling step in the population of polynucleotides, therefore quantifying the expression of the population of polynucleotides encoding the antibodies or T-cell receptors; and an oligonucleotide library (I) for sequencing by hybridization of polynucleotides encoding variable regions of antibodies or T cell receptors, comprising essentially of a set of overlapping oligonucleotides collectively selected to hybridize with all germline segments encoding the variable regions of the antibodies or T cell receptors under conditions allowing formation of hybridization duplexes between the set of overlapping oligonucleotides and the polynucleotides, and variant set of oligonucleotides of the overlapping oligonucleotides, which comprises (G, C, T, A) base variation in one or more positions of the overlapping oligonucleotides. (M1) is useful for sequencing a population of polynucleotides encoding antibodies or T-cell receptor. (M1) enables a high-throughput method of sequencing a population of polynucleotides that is having the ability to screen a broad spectrum of

CC samples, and allows the analysis of a large amount of cells and samples in a fast manner in order to identify a number of relevant target nucleic acids. This sequence represents a mutated human gene fragment VH1-18 associated with the sequencing method of the invention.

XX SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 44.0%; Score 8.8; DB 17; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16  
||| ||||| |||  
DB 12 CAGTTGAAGTTG 1

RESULT 107  
ID AEC62419/c  
XX AEC62419 standard; DNA; 12 BP.  
XX AC AEC62419;  
XX DT 17-NOV-2005 (first entry)  
XX DE Human gene fragment VH1-18 mutant SEQ ID NO 29.  
XX KW DNA sequencing; DNA amplification; DNA microarray; VH1-18; ds; mutant.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO2005084134-A2.  
XX PD 15-SEP-2005.  
XX PF 06-MAR-2005; 2005WO-IL000263.  
XX PR 04-MAR-2004; 2004US-0549541P.  
XX PA (LESH/) LESHKOWITZ D.  
XX PI Leshkowitz D;  
XX DR WPI; 2005-639011/65.  
XX PS Sequencing population of polynucleotide (PP) by forming hybridization duplex of known oligonucleotide and PP, detecting oligonucleotide involved in duplex formation and compiling set of sequences of PP.  
XX Example 1; SEQ ID NO 29; 102pp; English.  
XX The invention describes a method of sequencing (M1) a population of polynucleotides encoding antibodies or T-cell receptors, comprising contacting oligonucleotides of known sequences with population of polynucleotides, to allow formation of hybridization duplexes, quantitatively detecting oligonucleotides involved in formation of the hybridization duplexes and compiling set of sequences of the population of polynucleotides. Also described are: quantifying an expression of a population of polynucleotides encoding antibodies or T-cell receptors, comprising carrying out the steps of (M1), and determining a level of each set of the compiled set of sequences of assembling step in the population of polynucleotides, therefore quantifying the expression of the population of polynucleotides encoding the antibodies or T-cell receptors; and an oligonucleotide library (I) for sequencing by hybridization of polynucleotides encoding variable regions of antibodies or T cell receptors, comprising essentially of a set of overlapping oligonucleotides collectively selected to hybridize with all germline segments encoding the variable regions of the antibodies or T cell receptors under conditions allowing formation of hybridization duplexes between the set of overlapping oligonucleotides and the polynucleotides, and variant set of oligonucleotides of the overlapping oligonucleotides, which comprises (G, C, T, A) base variation in one or more positions of

CC the overlapping oligonucleotides. (M1) is useful for sequencing a  
 CC population of polynucleotides encoding antibodies or T-cell receptor.  
 CC (M1) enables a high-throughput method of sequencing a population of  
 CC polynucleotides that is having the ability to screen a population of  
 CC samples, and allows the analysis of a large amount of cells and samples  
 CC in a fast manner in order to identify a number of relevant target nucleic  
 CC acids. This sequence represents a mutated human gene fragment Vhl-18  
 CC associated with the sequencing method of the invention.

XX SQ Sequence 12 BP; 2 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 17; Length 12;  
 Score over Length 73.3%;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16

Db 12 CAGCTGAAGCTG 1

RESULT 108

AEL03638  
 ID AEL03638 standard; DNA; 12 BP.

XX AC AEL03638;

XX 30-NOV-2006 (first entry)

XX Human mitochondrial DNA, D-loop, probe SEQ ID NO:357.

XX DNA detection; DNA microarray; DNA chip; SNP detection; ss;  
 KW microorganism detection; cancer; cytostatic; neoplasm; infection;  
 KW antimicrobial; genetic disorder; mitochondrial genome; probe.

XX OS Homo sapiens.

XX US7115364-B1.

XX 03-OCT-2006.

XX 02-AUG-1995; 95US-00510521.

XX 26-OCT-1993; 93US-00143312.

XX 02-AUG-1994; 94US-00284064.

XX 26-OCT-1994; 94WO-US012305.

XX (AFFY-) AFFYMETRIX INC.

XX Chee M, Cronin MT, Fodor SPA, Gingeras TR, Huang XC, Hubbell EA;  
 PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;

XX WPI; 2006-706320/73.

XX Array of nucleic acid probes immobilized on solid support for comparing  
 PT target nucleic acid with reference sequence, has first probe set with  
 PT nucleotides complementary to reference, second probe set interrogated in  
 PT first probe set.

XX Disclosure; SEQ ID NO 357; 233pp; English.

XX The invention relates to an array of nucleic acid probes immobilized on a  
 CC solid support, the array comprising at least two sets or four sets of  
 CC probes: a first probe set comprising several probes, each probe  
 CC comprising a segment of at least six nucleotides exactly complementary to  
 CC a subsequence of a reference sequence, the segment including at least one  
 CC interrogation position complementary to a corresponding nucleotide in the  
 CC reference sequence; a second, third and fourth probe set comprising a  
 CC probe for each interrogation position in the first probe set, each probe  
 CC in the second probe set being identical to a subsequence comprising a  
 CC corresponding probe from the first probe set or a subsequence of at least  
 CC six nucleotides that includes the interrogation position, except that the  
 CC interrogation position is occupied by a different nucleotide in each of

CC the two corresponding probes from the first and second probe sets. The  
 CC probes in the first probe set collectively have at least three  
 CC interrogation positions respectively corresponding to each of three  
 CC contiguous nucleotides in the reference sequence, provided that the array  
 CC does not consist of a complete set of probes of a given length. A  
 CC complete set is all permutations of nucleotides A, C, G and T/U. The  
 CC reference sequence is at least 50 bases, and the first probe set  
 CC comprises overlapping probes spanning the reference sequence. Also  
 CC included are comparing a target nucleic acid with a reference sequence  
 CC comprising a predetermined sequence of nucleotides using the array of the  
 CC invention, hybridizing a sample comprising the target nucleic acid to an  
 CC array of nucleic acid probes immobilized on a solid support (the array  
 CC comprising a set of probes comprising a first probe comprising a segment  
 CC of at least 7 nucleotides exactly complementary to a subsequence of a  
 CC reference sequence except at one or two positions, the segment including  
 CC an interrogation position not at the one or two positions, second, third  
 CC and fourth mutant probes, each identical to a sequence comprising the  
 CC wild-type probe or a subsequence including the interrogation position and  
 CC the one or two positions, except in the interrogation position, which is  
 CC occupied by a different nucleotide in each of the four probes, provided  
 CC the array does not consist of a complete set of probes of a given length,  
 CC where a complete set is all permutations of nucleotides A, C, G and T/U),  
 CC identifying variants of a reference sequence differing from the reference  
 CC sequence in at least one nucleotide and a block of nucleic acid probes  
 CC immobilized on a solid support (the array comprising a wild-type probe  
 CC comprising a segment of at least six nucleotides exactly complementary to  
 CC a subsequence of a reference sequence, the segment having several  
 CC interrogation positions respectively corresponding to several nucleotides  
 CC in the reference sequence for each interrogation position, three mutant  
 CC probes, each identical to a sequence comprising the wild-type probe or a  
 CC subsequence of at least six nucleotides including the several  
 CC interrogation positions, except in the interrogation position, provided  
 CC the array does not consist of a complete set of probes of a given length,  
 CC where a complete set is all permutations of nucleotides A, C, G and T/U,  
 CC where the reference sequence is from a gene having a variant form  
 CC associated with development of cancer, a pathogenic microorganism, a  
 CC biotransformation gene, or a gene associated with a hereditary disorder).  
 CC The array of nucleic acid probes is useful for comparing target nucleic  
 CC acid with a reference sequence comprising a predetermined sequence of  
 CC nucleotides, where the reference sequence is a gene from an HIV virus,  
 CC cystic fibrosis transmembrane indicating receptor (CFTR) gene,  
 CC mitochondrial genome or biotransformation gene. The other reference  
 CC sequences include p34, p65 (implicated in breast, prostate and liver  
 CC cancer) and DNA segments encoding cytochromes P450 and other  
 CC biotransformation genes, these reference sequences have use for forensic  
 CC or epidemiological studies. Other reference sequences of interest include  
 CC p34 (related to p53), p65 (implicated in breast and liver cancer), and  
 CC DNA segments encoding. Other reference sequences of interest include  
 CC those from the genome of pathogenic viruses (e.g., hepatitis (A, B, or  
 CC C), herpes virus (e.g., VZV, HSV-1, HAV-6, HSV-II, and CMV, Epstein Barr  
 CC virus), adenovirus, influenza virus, flaviviruses, echovirus, rhinovirus,  
 CC genomes or episomes of pathogenic bacteria, such bacteria include  
 CC Chlamydia, Rickettsia, Mycobacterium, Staphylococcus, Streptococcus,  
 CC Pneumococcus, Klebsiella, Proteus, Serratia, Pseudomonas, and reference  
 CC sequences in which mutations result in sickle cell anemia, beta-  
 CC thalassemia, phenylketonuria, or galactosemia. The reference sequences  
 CC are useful in forensic or epidemiological studies. The array is useful to  
 CC read a target sequence comprising either the reference sequence itself or  
 CC its variants. The present sequence is a probe for a D-loop region of the  
 CC mitochondrial genome.

XX SQ Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 44.0%; Score 8.8; DB 19; Length 12;

Score over Length 73.3%;

Best Local Similarity 83.3%; Pred. No. 2.8e+06;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20

Db 1 TGAAGTTGCAGT 12



RESULT 109  
AEL03639  
ID AEL03639 standard; DNA; 12 BP.  
XX AC  
AC AEL03639;  
XX DT  
DT 30-NOV-2006 (first entry)  
XX  
XX Human mitochondrial DNA, D-loop, probe SEQ ID NO:358.  
XX  
XX DNA detection: DNA microarray; DNA chip; SNP detection; ss;  
KW microorganism detection; cancer; cytostatic; neoplasm; infection;  
KW antimicrobial; genetic disorder; mitochondrial genome; probe.  
XX OS  
OS Homo sapiens.  
XX  
XX US7115364-B1.  
XX PN  
XX  
XX 03-OCT-2006.  
XX PD  
XX  
XX 02-AUG-1995; 95US-00510521.  
XX PF  
XX  
XX 26-OCT-1993; 93US-00143312.  
XX PR  
XX 26-AUG-1994; 94US-00284064.  
XX PR  
XX 02-OCT-1994; 94WO-US012305.  
XX PR  
XX  
XX (AFFY-) AFFYMETRIX INC.  
XX PA  
XX  
XX Chee M, Cronin MT, Fodor SPA, Gingeras TR, Huang XC, Hubbell EA;  
PI Lipshutz RJ, Lobb PA, Miyada CG, Morris MS, Shah N, Sheldon EL;  
PI  
XX WPI; 2006-706320/73.  
XX DR  
XX  
XX Array of nucleic acid probes immobilized on solid support for comparing  
PT target nucleic acid with reference sequence, has first probe set with  
PT nucleotides complementary to reference, second probe set interrogated in  
PT first probe set.  
XX  
XX Disclosure; SEQ ID NO 358; 233pp; English.  
XX PS  
XX  
XX The invention relates to an array of nucleic acid probes immobilized on a  
CC solid support, the array comprising at least two sets or four sets of  
CC probes: a first probe set comprising several probes, each probe  
CC comprising a segment of at least six nucleotides exactly complementary to  
CC a subsequence of a reference sequence, the segment including at least one  
CC an interrogation position complementary to a corresponding nucleotide in the  
CC reference sequence; a second, third and fourth probe set comprising a  
CC probe for each interrogation position in the first probe set, each probe  
CC in the second probe set being identical to a sequence comprising a  
CC corresponding probe from the first probe set or a subsequence of at least  
CC six nucleotides that includes the interrogation position, except that the  
CC interrogation position is occupied by a different nucleotide in each of  
CC the two corresponding probes from the first and second probe sets. The  
CC probes in the first probe set collectively have at least three  
CC interrogation positions respectively corresponding to each of three  
CC contiguous nucleotides in the reference sequence, provided that the array  
CC does not consist of a complete set of probes of a given length. A  
CC complete set is all permutations of nucleotides A, C, G and T/U. The  
CC reference sequence is at least 50 bases, and the first probe set  
CC comprises overlapping probes spanning the reference sequence. Also  
CC included are comparing a target nucleic acid with a reference sequence  
CC comprising a predetermined sequence of nucleotides using the array of the  
CC array of nucleic acid probes immobilized on a solid support (the array  
CC comprising a set of probes comprising a first probe comprising a segment  
CC of at least 7 nucleotides exactly complementary to a subsequence of a  
CC reference sequence except at one or two positions, the segment including  
CC an interrogation position not at the one or two positions, second, third  
CC and fourth mutant probes, each identical to a sequence comprising the  
CC wild-type probe or a subsequence including the interrogation position and  
CC the one or two positions, except in the interrogation position, which is  
CC occupied by a different nucleotide in each of the four probes, provided  
CC the array does not consist of a complete set of probes of a given length,  
CC

CC	where a complete set is all permutations of nucleotides A, C, G and T/U).
CC	identifying variants of a reference sequence differing from the reference
CC	sequence in at least one nucleotide and a block of nucleic acid probes
CC	immobilized on a solid support (the array comprising a wild-type probe
CC	comprising a segment of at least six nucleotides exactly complementary to
CC	a subsequence of a reference sequence, the segment having several
CC	interrogation positions respectively corresponding to several nucleotides
CC	in the reference sequence for each interrogation position, three mutant
CC	probes, each identical to a sequence comprising the wild-type probe or a
CC	subsequence of at least six nucleotides including the several
CC	interrogation positions, except in the interrogation position, provided
CC	the array does not consist of a complete set of probes of a given length,
CC	where a complete set is all permutations of nucleotides A, C, G and T/U,
CC	where the reference sequence is from a gene having a variant form
CC	associated with development of cancer, a pathogenic microorganism, a
CC	biotransformation gene, or a gene associated with a hereditary disorder).
CC	The array of nucleic acid probes is useful for comparing target nucleic
CC	acid with a reference sequence comprising a predetermined sequence of
CC	nucleotides, where the reference sequence is a gene from an HIV virus,
CC	cystic fibrosis transmembrane indicating receptor (CFTR) gene,
CC	mitochondrial genome or biotransformation gene. The other reference
CC	sequences include p34, p65 (implicated in breast, prostate and liver
CC	cancer) and DNA segments encoding cytochromes P450 and other
CC	biotransformation genes; these reference sequences have use for forensic
CC	or epidemiological studies. Other reference sequences of interest include
CC	p34 (related to p53), p65 (implicated in breast and liver cancer), and
CC	DNA segments encoding. Other reference sequences of interest include
CC	those from the genome of pathogenic viruses (e.g., hepatitis (A, B, or
CC	C), herpes virus (e.g., VZV, HSV-1, HAV-6, HSV-II, and CMV, Epstein Barr
CC	virus), adenovirus, influenza virus, flaviviruses, echovirus, rhinovirus,
CC	genomes or episomes of pathogenic bacteria, such bacteria include
CC	Chlamydia, Rickettsia, Mycobacterium, Staphylococcus, Streptococcus,
CC	Pneumococcus, Klebsiella, Proteus, Serratia, Pseudomonas, and reference
CC	sequences in which mutations result in sickle cell anemia, beta-
CC	thalassaemia, phenylketonuria, or galactosemia. The reference sequences
CC	are useful in forensic or epidemiological studies. The array is useful to
CC	read a target sequence comprising either the reference sequence itself or
CC	its variants. The present sequence is a probe for a D-loop region of the
CC	mitochondrial genome.
XX	
SQ	Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
Query Match	44.0%; Score 8.8; DB 19; Length 12;
Score over Length	73.3%;
Best Local Similarity	83.3%; Pred. No. 2.8e+06;
Matches 10; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy	6 AGTTGAGATTGC 17
Db	
	1 ATTTGGAGTTGC 12
RESULT 110	
AEM30631	
ID	AEM30631 standard; RNA; 12 BP.
XX	
AC	AEM30631;
XX	
DT	08-MAR-2007 (first entry)
DE	
DE	E. coli rRNA sequence #37.
KW	RNA detection; fluorescence; protein production; bacterial infection;
KW	Escherichia coli infection; Pseudomonas aeruginosa infection; ss.
OS	Escherichia coli.
XX	
PN	WO2006122277-A2.
XX	
PD	16-NOV-2006.
PF	11-MAY-2006; 2006WO-US018320.
XX	



PR 11-MAY-2005; 2005US-0680138P.  
XX 25-AUG-2005; 2005US-0711492P.  
PA (UTWA-) UNIV WAYNE STATE.  
XX Cunningham PR;  
XX WPI; 2007-132103/13.  
XX  
XX New nucleic acids that are conserved and variable regions of Escherichia  
PT coli 16S rRNA, useful as targets for pharmaceuticals that are  
PT taxonomically specific and/or refractory for developing drug resistance.  
XX  
XX Example; Fig 5.10; 232pp; English.  
XX  
XX The invention relates to a nucleic acid represented by a specific  
CC formula. The invention also relates to a method of identifying an agent  
CC that binds to a nucleic acid, a method of identifying an inhibitor of  
CC protein synthesis, a compound obtained by the method and a method of  
CC administering a compound to a patient in need. Identifying an agent,  
CC which binds to a nucleic acid of the invention comprises measuring the  
CC fluorescence of the nucleic acid, thus establishing a first fluorescence  
CC reading, contacting a test compound with the nucleic acid and measuring  
CC the resulting fluorescence, thus establishing a second fluorescence  
CC reading, determining the difference between the first fluorescence  
CC reading and the second fluorescence reading and selecting the compound  
CC where the difference between the first fluorescence reading and the  
CC second fluorescence reading is non-zero, thus identifying the agent. It  
CC further comprises modifying the agent identified, thus forming a modified  
CC agent, contacting the modified agent with the nucleic acid and measuring  
CC the resulting fluorescence, thus establishing a modified second  
CC fluorescence reading, determining the difference between the first  
CC fluorescence reading and the modified second fluorescence reading and  
CC selecting the compound where the difference between the first  
CC fluorescence reading and the second modified fluorescence reading is non-  
CC zero, thus identifying a modified agent. Assaying the inhibitory  
CC properties of the agent comprises detecting protein synthesis or  
CC determining the inhibitor constant for inhibiting mRNA translation. The  
CC nucleic acids are conserved and can be used as targets for  
CC pharmaceuticals that are taxonomically specific, refractory to the  
CC development of drug resistance or both. They can also be used for  
CC identifying an inhibitor of protein synthesis. The compound can be  
CC administered to a patient having a microbial infection, preferably a  
CC bacterial infection, e.g. E. coli or Pseudomonas aeruginosa infection.  
XX This sequence represents E. coli rRNA used in the scope of the invention.  
XX  
SQ Sequence 12 BP; 3 A; 2 C; 4 G; 0 T; 3 U; 0 Other;  
  
Query Match 44.0%; Score 8.8; DB 22; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 58.3%; Pred. No. 2.8e+06;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 5 CAGTTGAAGTTC 16  
Db 1 CAGGUGAACUUG 12  
  
RESULT 111  
AGD66526/c  
ID AGD66526 standard; DNA; 12 BP.  
XX  
XX AGD66526;  
AC  
XX  
XX 23-AUG-2007 (first entry)  
XX Human target DNA, SEQ ID: 7.  
DE  
XX  
XX DNA detection; electrophoresis; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2007138013-A1.  
FN  
  
XX 21-JUN-2007.  
XX  
XX 25-OCT-2006; 2006US-00585939.  
XX  
XX 26-OCT-2005; 2005JP-00311933.  
XX (HAYA/) HAYASHI M.  
PA (MORI/) MORI K.  
PA (MAED/) MAEDA M.  
XX  
XX Hayashi M, Mori K, Maeda M;  
PI  
XX WPI; 2007-524355/51.  
DR  
XX  
XX New separation device comprising electrodes, useful for DNA separation by  
PT electrophoresis.  
PT  
XX Disclosure; SEQ ID NO 7; 21pp; English.  
PS  
XX The present invention provides a DNA separation device for separating  
CC first sample DNA and second sample DNA by electrophoresis, the device  
CC comprising a positive electrode and a negative electrode, a conjugate DNA  
CC solution, and a presample solution, voltage applied to the electrodes and  
CC thereby separating the DNA complexes. The invention is useful for  
CC detecting a difference in portions of base sequences of DNAs and a ligand  
CC DNA. The present sequence is a human target DNA from first sample DNA 5.  
XX  
XX Sequence 12 BP; 0 A; 3 C; 6 G; 3 T; 0 U; 0 Other;  
SQ  
  
Query Match 44.0%; Score 8.8; DB 22; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2 CCCGAGTTCGAG 13  
Db 12 CCCGAGCCGAG 1  
  
RESULT 112  
AAF05404/c  
ID AAF05404 standard; DNA; 17 BP.  
XX  
XX AAF05404;  
AC  
XX  
XX 16-FEB-2001 (first entry)  
DT  
XX  
XX Hammerhead ribozyme substrate #2623.  
DE  
XX  
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
KW interferon alpha; ss.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2000061729-A2.  
PN  
XX  
XX 19-OCT-2000.  
PD  
XX  
XX 11-APR-2000; 2000WO-US009721.  
PF  
XX  
XX 12-APR-1999; 99US-0129390P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX  
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;  
PI  
XX  
XX WPI; 2000-647423/62.  
DR  
XX  
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
PT useful for producing e.g. granulocyte colony stimulating factor protein,  
PT interferon alpha and erythropoietin.  
XX

PS Claim 18; Page 116; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid  
CC molecules that act as inhibitors of the expression of repressor genes  
CC encoding the TP2 Orphan receptor, EAR3/COUP-TP-1, the GATA transcription  
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).  
CC Inhibition of the repressors removes prevents inhibition (and  
CC consequently increases expression of) genes involved in the production of  
CC erythropoietin, granulocyte colony stimulating factor protein and  
CC interferon alpha

XX Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

SQ Query Match 62.0%; Score 12.4; DB 3; Length 17;  
Score over Length 72.9%;  
Best Local Similarity 92.9%; Pred. No. 5e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17  
DB 15 CCAGTTGAAGCTGC 2

RESULT 113  
AAPO5403/C  
ID AAF05403 standard; DNA; 17 BP.

XX AAF05403;

XX 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #3622.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;

KW interferon alpha; ss.

XX Homo sapiens.

XX WO200061729-A2.

XX 19-OCT-2000.

XX 11-APR-2000; 2000WO-US009721.

XX 12-APR-1999; 99US-0129390P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Zwick M, Pavco P, Mcswiggen J;

XX WPI; 2000-647423/62.

XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
PT useful for producing e.g. granulocyte colony stimulating factor protein,  
PT interferon alpha and erythropoietin.

XX Claim 18; Page 116; 164pp; English.

XX The present invention relates to enzymatic and antisense nucleic acid  
CC molecules that act as inhibitors of the expression of repressor genes  
CC encoding the TP2 Orphan receptor, EAR3/COUP-TP-1, the GATA transcription  
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).  
CC Inhibition of the repressors removes prevents inhibition (and  
CC consequently increases expression of) genes involved in the production of  
CC erythropoietin, granulocyte colony stimulating factor protein and  
CC interferon alpha

XX Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

SQ Query Match 62.0%; Score 12.4; DB 3; Length 17;  
Score over Length 72.9%;  
Best Local Similarity 92.9%; Pred. No. 5e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGC 17  
DB 16 CCAGTTGAAGCTGC 3

RESULT 114  
AEH24548/c  
ID AEH24548 standard; DNA; 22 BP.

XX AEH24548;

AC 29-JUN-2006 (first entry)

DT BAX gene forward PCR primer.

DE ss; PCR; primer; drug metabolism; cancer; cytostatic; neoplasm;

XX immune inhibition; apoptosis stimulation; RNA quantitation; BAX.

XX Homo sapiens.

XX WO2006045053-A2.

XX 27-APR-2006.

XX 20-OCT-2005; 2005WO-US037925.

XX 20-OCT-2004; 2004US-0620603P.

XX 16-FEB-2005; 2005US-0653557P.

XX 08-JUN-2005; 2005US-0688741P.

XX (HITB ) HITACHI CHEM CO LTD.  
(HITB ) HITACHI CHEM RES CENT INC.

XX Mitsuhashi M;

XX WPI; 2006-332057/34.

XX Measuring a patient's responsiveness to a drug comprises exposing whole  
PT blood of the patient to the drug for 7 hours or less, and measuring the  
PT amount of an mRNA associated with an effect of the drug in blood cells.

XX Disclosure; SEQ ID NO 39; 74pp; English.

XX The invention relates to a method of measuring a patient's responsiveness  
CC to a which drug comprises exposing whole blood of the patient to the drug  
CC for 7 hours or less, and measuring the amount of an mRNA associated with  
CC an effect of the drug in blood cells. Preferably, the amount of the mRNA  
CC present in the blood cells is measured before the exposure, and the  
CC change in the amount of the mRNA is determined by comparing the amount of  
CC mRNA measured before exposure to the amount of mRNA measured after  
CC exposure. The method additionally comprises exposing whole blood of the  
CC patient to a control vehicle for 7 hours or less; after the exposure,  
CC measuring the amount of the mRNA associated with an effect of the drug in  
CC the blood cells exposed to the control vehicle; and identifying  
CC responsiveness to the drug includes comparing results of the measurement  
CC obtained after exposure to the control vehicle with results of the  
CC measurement obtained after exposure to the drug. The control vehicle is  
CC selected from phosphate-buffered saline and dimethyl sulfoxide. The mRNA  
CC is selected from mRNAs encoding the gene products of the Bcl-2/Bax gene  
CC family, Bax gene product, the Bcl-2 gene family, ATP-binding  
CC cassette subfamilies A to G, and p21, PUMA and NOXA gene products. The  
CC method is useful for measuring a patient's responsiveness to a drug,  
CC which is useful in developing an optimized treatment protocol tailored to  
CC the specific patient. The method may be used for patients with conditions  
CC such as cancer or diseases which require immunosuppression. The present  
CC sequence represents BAX gene forward PCR primer. This gene was amplified  
CC in studies of drug induced apoptosis in tailored drug administration for  
CC leukemia and lymphoma.

XX Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

SQ Query Match 80.0%; Score 16; DB 19; Length 22;

Score over Length 72.7%; Pred. No. 8.9e+02; DB 19; Length 22;  
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20  
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 115  
AEH24560/c  
ID AEH24560 standard; DNA; 22 BP.  
AC AEH24560;  
XX  
DT 29-JUN-2006 (first entry)  
XX  
DE BAX forward real-time PCR primer.  
XX  
KW ss; PCR; primer; drug metabolism; cancer; cytostatic; neoplasm;  
KW immune inhibition; apoptosis stimulation; RNA quantitation; BAX.  
XX  
OS Homo sapiens.  
XX  
PN WO2006045053-A2.  
XX  
PD 27-APR-2006.  
XX  
PP 20-OCT-2005; 2005WO-US037925.  
XX  
PR 20-OCT-2004; 2004US-0620603P.  
PR 16-FEB-2005; 2005US-0653557P.  
PR 08-JUN-2005; 2005US-0688741P.  
XX  
PA (HITB ) HITACHI CHEM CO LTD.  
PA (HITB ) HITACHI CHEM RES CENT INC.  
XX  
PI Mitsuhashi M;  
XX  
DR WPI; 2006-332057/34.  
XX  
PT Measuring a patient's responsiveness to a drug comprises exposing whole  
PT blood of the patient to the drug for 7 hours or less, and measuring the  
PT amount of an mRNA associated with an effect of the drug in blood cells.  
XX  
PS Disclosure; SEQ ID NO 51; 74pp; English.  
XX  
CC The invention relates to a method of measuring a patient's responsiveness  
CC to a which drug comprises exposing whole blood of the patient to the drug  
CC for 7 hours or less, and measuring the amount of an mRNA associated with  
CC an effect of the drug in blood cells. Preferably, the amount of the mRNA  
CC present in the blood cells is measured before the exposure, and the  
CC change in the amount of the mRNA is determined by comparing the amount of  
CC mRNA measured before exposure to the amount of mRNA measured after  
CC exposure. The method additionally comprises exposing whole blood of the  
CC patient to a control vehicle for 7 hours or less; after the exposure,  
CC measuring the amount of the mRNA associated with an effect of the drug in  
CC the blood cells exposed to the control vehicle; and identifying  
CC responsiveness to the drug includes comparing results of the measurement  
CC obtained after exposure to the control vehicle with results of the  
CC measurement obtained after exposure to the drug. The control vehicle is  
CC selected from phosphate-buffered saline and dimethyl sulfoxide. The mRNA  
CC is selected from mRNAs encoding the gene products of the Bcl-2/Bax gene  
CC family, Bax gene product, the BH3-only Bcl-2 gene family, ATP-binding  
CC cassette subfamilies A to G, and p21, PUMA and NOXA gene products. The  
CC method is useful for measuring a patient's responsiveness to a drug,  
CC which is useful in developing an optimized treatment protocol tailored to  
CC the specific patient. The method may be used for patients with conditions  
CC such as cancer or diseases which require immunosuppression. The present  
CC sequence represents BAX forward real-time PCR primer, used in RNA  
CC quantitation of BAX in assessment of leukocyte suppression.  
XX  
SQ Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 19; Length 22;  
Score over Length 72.7%;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20  
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 116  
AEJ10474/c  
ID AEJ10474 standard; DNA; 22 BP.  
XX  
AC AEJ10474;  
XX  
DT 07-SEP-2006 (first entry)  
XX  
DE Antisense PCR primer for RCR from 3-way junction structure.  
XX  
KW DNA detection; microorganism detection; SNP detection;  
KW epigenetic modification; diagnostic; RNA detection; DNA amplification;  
KW DNA methylation; gene amplification; primer extension; primer; PCR;  
KW antisense; ss.  
XX  
OS Synthetic.  
XX  
PN WO2006074162-A2.  
XX  
PD 13-JUL-2006.  
XX  
PP 04-JAN-2006; 2006WO-US000086.  
XX  
PR 04-JAN-2005; 2005US-0641255P.  
PR 14-JUL-2005; 2005US-0699340P.  
XX  
PA (HITB ) HITACHI CHEM CO LTD.  
PA (HITB ) HITACHI CHEM RES CENT INC.  
XX  
PI Murakami T;  
XX  
DR WPI; 2006-513365/52.  
XX  
PT Amplifying nucleic acid, by combining a nucleic acid primer with a  
PT polymerase and a circular nucleic acid probe, and producing a repeat of a  
PT sequence copy of the circular nucleic acid probe.  
XX  
PS Example 2; SEQ ID NO 6; 34pp; English.  
XX  
CC The present invention discloses a method of amplifying nucleic acid using  
CC primers and probes by rolling circle amplification method. The present  
CC invention comprises primer generation ? rolling circle amplification (PG-  
CC RCA) in which a ribbon probe is involved, allows the single step  
CC detection of nucleic acid sequences such as DNA and RNA sensitively and  
CC rapidly. This technology is easily applicable to detection of other  
CC biomolecules such as DNA methylation, single nucleotide polymorphism  
CC (SNP), protein and posttranslational modifications. PGR (primer  
CC generation reaction) is a reaction that is designed to produce at least  
CC one nucleic acid primer from a PGR initiation sequence of an RCR (rolling  
CC circle reaction) product and the resulting primer is designed to prime to  
CC a circular nucleic acid probe and initiate RCR. On the other hand, RCR is  
CC designed to produce concatenated sequence copies of the circular probe,  
CC in which the resulting product contains at least one PGR initiation  
CC sequence in every repeat sequence just like the initial reaction signal.  
CC The first and second nucleic acid primers are generated by one of  
CC cleavage-based cleavage reaction, strand displacement amplification,  
CC cleavage-initiated isothermal amplification, three-way junction  
CC isothermal amplification, three-way junction rolling circle reaction,  
CC binding assay using a nucleic acid labeled recognition agent and  
CC proximity assay. The method of nucleic acid detection using the present  
CC invention is useful for in vitro diagnostics and in pathogen detection.  
XX  
CC The nucleotide sequence presented here is the antisense PCR primer for

```
CC RCR from 3-way junction structure.
SQ Sequence 22 BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match      80.0%; Score 16; DB 19; Length 22;
  Score over Length 72.7%;
  Best Local Similarity 100.0%; Pred. No. 8.9e+02;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20
DB 22 CAGTTGAAGTTGCCGT 7

RESULT 117
ABC96949/c
ID ABC96949 standard; DNA; 13 BP.
XX
AC ABC96949;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 96966 for detecting SNP TSC0024054.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 96966; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 13;
  Score over Length 72.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
DB 13 TGAAGTTGCCG 3

RESULT 118
ABC25038
ID ABC25038 standard; DNA; 13 BP.
XX
AC ABC25038;
XX
XX 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 25055 for detecting SNP TSC0006071.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 25055; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match      47.0%; Score 9.4; DB 5; Length 13;
  Score over Length 72.3%;
  Best Local Similarity 90.9%; Pred. No. 1.4e+06;
  Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
DB 3 TGAAGTTGCCG 13

RESULT 119
ABF17290
ID ABF17290 standard; DNA; 13 BP.
XX
AC ABF17290;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 117287 for detecting SNP TSC0029345.
XX
```

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 117287; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
DB 3 AGTTGAGTTG 13  
RESULT 120  
ABF17291/C  
ID ABF17291 standard; DNA; 13 BP.  
XX  
XX AC ABF17291;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 117288 for detecting SNP TSC0029345.  
DE  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX

PR 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 117288; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
DB 11 AGTTGAGTTG 1  
RESULT 121  
ABF17512  
ID ABF17512 standard; DNA; 13 BP.  
XX  
XX AC ABF17512;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 117509 for detecting SNP TSC0029385.  
DE  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX

PS Claim 1; SEQ ID NO 117509; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
DB 3 AGTTGAAGTTG 13  
RESULT 122  
ID ABC27952 standard; DNA; 13 BP.  
XX  
AC ABC27952;  
XX  
DT 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 27969 for detecting SNP TSC0007879.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 27969; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
DB 3 AGTTGAAGTTG 13  
RESULT 123  
ID ABH35811/C standard; DNA; 13 BP.  
XX  
AC ABH35811;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 235788 for detecting SNP TSC0009202.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 235788; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
DB 1 AGTTGAAGTTG 11

```

Db      13 AGTGAAGTTG 3

RESULT 124
ABF11324
ID      ABF11324 standard; DNA; 13 BP.
XX
AC      ABF11324;
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 111321 for detecting SNP TSC0027809.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 111321; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match      47.0%; Score 9.4; DB 5; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 1.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      6 AGTGAAGTTG 16
        ||||| |||||
Db      1 AGTTGTAGTTG 11

RESULT 126
ABH48372
ID      ABH48372 standard; DNA; 13 BP.
XX
AC      ABH48372;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 248349 for detecting SNP TSC0060684.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX

```



XX 07-APR-2000; 2000DE-01019173.  
XX (EPiG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX Claim 1; SEQ ID NO 248349; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences

XX Query Match 47.0%; Score 9.4; DB 5; Length 13;  
XX Score over Length 72.3%;  
XX Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX Qy 6 AGTTGAAGTTG 16  
XX Db 1 AGTTGAGTTG 11

RESULT 127  
ABC25065/C  
ID ABC25065 standard; DNA; 13 BP.  
XX AC ABC25065;  
XX DT 20-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 25082 for detecting SNP TSC0006096.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPiG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.

XX Claim 1; SEQ ID NO 248349; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences

XX Query Match 47.0%; Score 9.4; DB 5; Length 13;  
XX Score over Length 72.3%;  
XX Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX Qy 6 AGTTGAAGTTG 16  
XX Db 1 AGTTGAGTTG 11

RESULT 128  
ABC06232  
ID ABC06232 standard; DNA; 13 BP.  
XX AC ABC06232;  
XX DT 20-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 6223 for detecting SNP TSC0001948.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPiG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.

XX Claim 1; SEQ ID NO 6223; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences



CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTTG 16  
|||||  
Db 3 AGTAGAAGTTG 13

RESULT 129  
ABC25039/C  
ID ABC25039 standard; DNA; 13 BP.

XX AC ABC25039;  
XX DT 20-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 25056 for detecting SNP TSC0006071.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.

XX PN WO200177384-A2.  
XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX PS Claim 1; SEQ ID NO 25056; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 5 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 TGAAGTTGCG 19

Db 11 TGAAGTTGCG 1  
|||||

RESULT 130  
ABC56736

ID ABC56736 standard; DNA; 13 BP.

XX AC ABC56736;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 56753 for detecting SNP TSC0015377.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX PS Claim 1; SEQ ID NO 56753; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTTG 16

|||||  
Db 1 AGTTGAAGTTG 11

RESULT 131  
ABC96948

ID ABC96948 standard; DNA; 13 BP.

XX AC ABC96948;

XX DT 21-FEB-2002 (first entry)

XX



PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 36538; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 AGTTGAAGTTG 16  
Db 13 ATTGAAGTTG 3  
  
RESULT 134  
ABH48373/C  
ID ABH48373 standard; DNA; 13 BP.  
XX  
AC ABH48373;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 248350 for detecting SNP TSC0060684.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is PT designed to detect single-nucleotide polymorphisms and cytosine PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 248350; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 AGTTGAAGTTG 16  
Db 13 ATTGAAGTTG 3  
  
RESULT 135  
ABC36520  
ID ABC36520 standard; DNA; 13 BP.  
XX  
AC ABC36520;  
XX  
XX 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 36537 for detecting SNP TSC0011456.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is PT designed to detect single-nucleotide polymorphisms and cytosine PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 36537; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



XX PF 06-APR-2001; 2001WO-IB0000713.  
XX XX  
PR 07-APR-2000; 2000DE-01019173.  
XX XX  
PA (EPiG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 215786; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
DB 13 AGTTGAGTTG 3  
RESULT 139  
ABC25064  
ID ABC25064 standard; DNA; 13 BP.  
AC ABC25064;  
XX  
XX 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 25081 for detecting SNP TSC0006096.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
FN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
FN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
PA (EPiG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 215786; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
DB 13 AGTTGAGTTG 3  
RESULT 140  
ABF17513/C  
ID ABF17513 standard; DNA; 13 BP.  
XX  
AC ABF17513;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 117510 for detecting SNP TSC0029385.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
FN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
PA (EPiG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 117510; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
DB 2 AGTTGAAGTTG 12

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
DB 11 AGTTGAAGTTG 1

RESULT 141  
ABH35810  
ID ABH35810 standard; DNA; 13 BP.

XX AC ABH35810;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 235787 for detecting SNP TSC0009202.

XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 235787; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
DB 1 AGTTGAAGTTG 11

RESULT 142  
ABC12623/C

XX ID ABC12623 standard; DNA; 13 BP.

XX AC ABC12623;

XX DT 20-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 12630 for detecting SNP TSC0002968.

XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 12630; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
DB 12 AGTTGAAGTTG 2

RESULT 143  
ABF11325/C

XX ID ABF11325 standard; DNA; 13 BP.

XX AC ABF11325;

XX

```
DT 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 111322 for detecting SNP TSC0027809.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 111322; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -AB09989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 47.0%; Score 9.4; DB 5; Length 13;
XX Score over Length 72.3%;
XX Best Local Similarity 90.9%; Pred. No. 1.4e+06;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 6 AGTTGAAGTTG 16
XX Db 11 AGTTGACTTG 1
XX
XX RESULT 144
XX ABC27953/C
XX ID ABC27953 standard; DNA; 13 BP.
XX
XX AC ABC27953;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 27970 for detecting SNP TSC0007879.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 111322; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -AB09989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 47.0%; Score 9.4; DB 5; Length 13;
XX Score over Length 72.3%;
XX Best Local Similarity 90.9%; Pred. No. 1.4e+06;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 6 AGTTGAAGTTG 16
XX Db 11 AGTTGACTTG 1
XX
XX RESULT 144
XX ABC27953/C
XX ID ABC27953 standard; DNA; 13 BP.
XX
XX AC ABC27953;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 27970 for detecting SNP TSC0007879.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 27970; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -AB09989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 47.0%; Score 9.4; DB 5; Length 13;
XX Score over Length 72.3%;
XX Best Local Similarity 90.9%; Pred. No. 1.4e+06;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 6 AGTTGAAGTTG 16
XX Db 13 AGTTGAAGTTG 3
XX
XX RESULT 145
XX ABC06233/C
XX ID ABC06233 standard; DNA; 13 BP.
XX
XX AC ABC06233;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 6224 for detecting SNP TSC0001948.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX
```

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 6224; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABJ00010-ABJ99989  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16

|||||  
11 AGTAGAAGTTG 1

RESULT 146

ABF87031/C  
ID ABF87031 standard; DNA; 13 BP.

XX ABF87031;

DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 187028 for detecting SNP TSC0046102.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPICENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 187028; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABJ00010-ABJ99989  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 5; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16

|||||  
13 AGTTGAAGTGG 3

RESULT 147

ADR35833/C  
ID ADR35833 standard; DNA; 13 BP.

XX ADR35833;

DT 04-NOV-2004 (first entry)

XX Human nicking agent DNA containing BstNBI restriction site #2253.

XX ss; nicking agent; assay panel; diagnosis; expression pattern;

KW DNA fingerprinting; nosocomial infection; microbiological assay;

KW bacterial contamination; genome mapping; bioremediation.

XX Homo sapiens.

XX WO2004067765-A2.

XX 12-AUG-2004.

XX 29-JAN-2004; 2004WO-US002720.

XX 29-JAN-2003; 2003US-0443811P.

XX (KECK-) KECK GRADUATE INST.

XX Van Ness J, Galas DJ, Van Ness LK;

XX WPI; 2004-581010/56.

XX Identifying nucleic acid sample source, useful for identifying bacterial  
PT strains involved in nosocomial infections, comprises treating the nucleic  
PT acid sample with components comprising a nicking agent under nicking  
PT conditions.

XX Example 3; Page 105-219; 238pp; English.

XX The invention relates to a method of treating a nucleic acid sample with  
CC components under nicking conditions, where the components comprise a  
CC nicking agent, and the conditions cause the nicking agent to nick the  
CC nucleic acid sample to thus produce a family of initiating  
CC oligonucleotide fragments, and subjecting one or more members of the  
CC family of initiating oligonucleotide fragments to a characterizing  
CC process to thus provide results. The method is useful for creating an  
CC assay panel of diagnostic oligonucleotides that can identify any organism  
CC or individual. The method is useful for characterizing other DNA  
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
CC The method, kit or composition is useful for identifying the source  
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
CC non-human animal or human. The method is particularly useful for rapidly  
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
CC subspecies, and especially strains or individuals of the subspecies. It  
CC is especially useful for identifying different bacterial strains involved  
CC in e.g., nosocomial infections. Furthermore, the method is useful for



CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring quality assurance/quality control of  
 CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-  
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI  
 CC restriction site and used in the method of the invention.

SQ Sequence 13 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 1 Other;  
 Query Match 47.0%; Score 9.4; DB 13; Length 13;  
 Score over Length 72.3%;  
 Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13  
 ||||| |||||  
 Db 13 CCCAGTSGAAG 3

RESULT 148  
 ADR35834/c  
 ID ADR35834 standard; DNA; 13 BP.

XX ADR35834;

DT 04-NOV-2004 (first entry)

DE Human nicking agent DNA containing BstNBI restriction site #2254.

XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.

XX Homo sapiens.

XX WO2004067765-A2.

XX 12-AUG-2004.

XX 29-JAN-2004; 2004WO-US002720.

XX 29-JAN-2003; 2003US-0443811P.

XX (KECK-) KECK GRADUATE INST.

XX Van Ness J, Galas DJ, Van Ness LK;

XX WPI; 2004-581010/56.

XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT strains involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.

XX Example 3; Page 105-219; 238pp; English.

XX The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the  
 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly

CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring quality assurance/quality control of  
 CC bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-  
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI  
 CC restriction site and used in the method of the invention.

SQ Sequence 13 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 1 Other;

Query Match 47.0%; Score 9.4; DB 13; Length 13;  
 Score over Length 72.3%;  
 Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13  
 ||||| |||||  
 Db 13 CCCAGTSGAAG 3

RESULT 149

ADR35835/c  
 ID ADR35835 standard; DNA; 13 BP.

XX ADR35835;

XX 04-NOV-2004 (first entry)

DE Human nicking agent DNA containing BstNBI restriction site #2255.

XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.

XX Homo sapiens.

XX WO2004067765-A2.

XX 12-AUG-2004.

XX 29-JAN-2004; 2004WO-US002720.

XX 29-JAN-2003; 2003US-0443811P.

XX (KECK-) KECK GRADUATE INST.

XX Van Ness J, Galas DJ, Van Ness LK;

XX WPI; 2004-581010/56.

XX Identifying nucleic acid sample source, useful for identifying bacterial  
 PT strains involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.

XX Example 3; Page 105-219; 238pp; English.

XX The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the  
 CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA

CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species.  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring quality assurance/quality control of  
 CC laboratory tests involving microbiological assays, tracing bacterial  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-  
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI  
 CC restriction site and used in the method of the invention.  
 XX  
 SQ Sequence 13 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 1 Other;

Query Match 47.0%; Score 9.4; DB 13; Length 13;  
 Score over Length 72.3%;  
 Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13  
 ||||| ||||  
 Db 13 CCCAGTGAAG 3

RESULT 150  
 ADR35832/c  
 ID ADR35832 standard; DNA; 13 BP.  
 XX  
 AC ADR35832;  
 DT 04-NOV-2004 (first entry)  
 XX Human nicking agent DNA containing BstNBI restriction site #2252.  
 XX ss; nicking agent; assay panel; diagnosis; expression pattern;  
 KW DNA fingerprinting; nosocomial infection; microbiological assay;  
 KW bacterial contamination; genome mapping; bioremediation.  
 XX  
 OS Homo sapiens.  
 PN WO2004067765-A2.  
 PD 12-AUG-2004.  
 XX 29-JAN-2004; 2004WO-US0002720.  
 PF 29-JAN-2003; 2003US-0443811P.  
 PR (KECK-) KECK GRADUATE INST.  
 PA Van Ness J, Galas DJ, Van Ness LX;  
 XX WPI; 2004-581010/56.  
 DR Identifying nucleic acid sample source, useful for identifying bacterial  
 XX strains involved in nosocomial infections, comprises treating the nucleic  
 PT acid sample with components comprising a nicking agent under nicking  
 PT conditions.  
 XX Example 3; Page 105-219; 238pp; English.  
 PS The invention relates to a method of treating a nucleic acid sample with  
 CC components under nicking conditions, where the components comprise a  
 CC nicking agent, and the conditions cause the nicking agent to nick the  
 CC nucleic acid sample to thus produce a family of initiating  
 CC oligonucleotide fragments, and subjecting one or more members of the

CC family of initiating oligonucleotide fragments to a characterization  
 CC process to thus provide results. The method is useful for creating an  
 CC assay panel of diagnostic oligonucleotides that can identify any organism  
 CC or individual. The method is useful for characterizing other DNA  
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
 CC The method, kit or composition is useful for identifying the source  
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
 CC non-human animal or human. The method is particularly useful for rapidly  
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,  
 CC subspecies, and especially strains or individuals of the subspecies. It  
 CC is especially useful for identifying different bacterial strains involved  
 CC in e.g., nosocomial infections. Furthermore, the method is useful for  
 CC diagnosing bacterial disease in plants and humans, monitoring for  
 CC bacterial content and/or contamination in the environment, monitoring  
 CC food for bacterial contamination, monitoring quality assurance/quality control of  
 CC bacterial contamination, monitoring microbiological assays, tracing bacterial  
 CC laboratory tests involving microbiological assays, genome mapping,  
 CC contamination and/or outbreaks of bacterial infections, genome mapping,  
 CC monitoring bioremediation sites, and for monitoring agricultural sites  
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-  
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI  
 CC restriction site and used in the method of the invention.  
 XX

SQ Sequence 13 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 1 Other;  
 Query Match 47.0%; Score 9.4; DB 13; Length 13;  
 Score over Length 72.3%;  
 Best Local Similarity 90.9%; Pred. No. 1.4e+06;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13  
 ||||| ||||  
 Db 13 CCCAGTGAAG 3

RESULT 151  
 ADQ80013/c  
 ID ADQ80013 standard; DNA; 17 BP.  
 XX  
 AC ADQ80013;  
 XX 09-SEP-2004 (first entry)  
 DT A. Kurodai octopamine receptor associated primer #8.  
 DE ss; PCR; primer; octopamine receptor; PKA pathway;  
 KW CAMP-dependent protein kinase; short-term memory.  
 XX Synthetic.  
 OS KR2004019613-A.  
 PN 06-MAR-2004.  
 PD 28-AUG-2002; 2002KR-00051211.  
 PF 28-AUG-2002; 2002KR-00051211.  
 PR (UYSE-) UNIV SEOUL NAT IND FOUND.  
 XX Jang DJ, Kang BG;  
 XX WPI; 2004-456652/44.  
 DR Octopamine receptor isolated from aplysia kurodai and activation method  
 PT of pka (camp-dependent protein kinase) pathway.  
 XX Disclosure; SEQ ID NO 8; 32pp; Korean.  
 PS The invention relates to an octopamine receptor isolated from Aplysia  
 CC kurodai and an activation method of PKA (CAMP-dependent protein kinase)  
 CC pathway. The method improves short-term memory and screens a drug  
 CC activating the PKA pathway to improve memory. The present sequence

CC represents an A. kurodai octopamine receptor associated primer.

SQ Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 13; Length 17;  
Score over Length 71.8%;  
Best Local Similarity 82.4%; Pred. No. 6.3e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCCGAGTTGAGTTGCC 18  
| | | | | | | | | | | | | | | | | |  
Db 17 CACGAGTTGAGTAGCC 1

## RESULT 152

AAQ83300  
ID AAQ83300 standard; DNA; 14 BP.

XX AC AAQ83300;

XX DT 25-MAR-2003 (revised).

XX DT 20-SEP-1995 (first entry)

XX DE c-jun antisense oligonucleotide.

XX KW c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;  
XX KW phosphorothioate; ss.

XX OS Synthetic.

XX PN WO9502051-A2.

XX PD 19-JAN-1995.

XX PF 06-JUL-1994; 94WO-EP002218.

XX PR 10-JUL-1993; 93EP-00111059.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;

XX DR WPI; 1995-066896/09.

XX Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and  
XX PT treating neuronal injury, degeneration, cell death and/or neoplasms.

XX PS Claim 2; Page 30; 86pp; English.

XX Antisense nucleic acid hybridising with an area of the mRNA and/or DNA  
XX CC comprising the genes c-jun, jun-B or c-fos, expression of which plays a  
XX CC causal role in neuronal injury, degeneration, cell death and/or  
XX CC neoplasms, can be used to prevent and treat such conditions. c-jun  
XX CC antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B  
XX CC antisense sequences are described in AAQ83322-363 and AAQ83444-45; and c-  
XX CC fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.  
XX CC Preferably the antisense sequences are phosphorothioate oligonucleotides  
XX CC since these are not destroyed as fast by endogenous factors as naturally  
XX CC occurring molecules. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 14 BP; 2 A; 1 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 2; Length 14;  
Score over Length 71.4%;  
Best Local Similarity 100.0%; Pred. No. 7.3e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
| | | | | | | | | | | | | | | | | |  
Db 5 GTTGAAGTTG 14

## RESULT 153

## AEJ10477

XX ID AEJ10477 standard; DNA; 24 BP.

XX AC AEJ10477;

XX DT 07-SEP-2006 (first entry)

XX DE Target nucleic acid for nuclease-based cleavage reaction PG-RCA.

XX KW DNA detection; microorganism detection; SNP detection;  
XX KW epigenetic modification; diagnostic; RNA detection; DNA amplification;  
XX KW DNA methylation; gene amplification; primer extension; ss;  
XX KW DNA-RNA hybrid.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
XX FT modified\_base 22..24  
XX FT /tag= a  
XX FT /mod\_base= 2'-O-methyluridine

XX PN WO2006074162-A2.

XX PD 13-JUL-2006.

XX PF 04-JAN-2006; 2006WO-US000086.

XX PR 04-JAN-2005; 2005US-0641255P.

XX PR 14-JUL-2005; 2005US-0699340P.

XX PA (HITB ) HITACHI CHEM CO LTD.

XX PA (HITB ) HITACHI CHEM RES CENT INC.

XX PI Murakami T;

XX DR WPI; 2006-513365/52.

XX PT Amplifying nucleic acid, by combining a nucleic acid primer with a  
XX PT polymerase and a circular nucleic acid probe, and producing a repeat of a  
XX PT sequence copy of the circular nucleic acid probe.

XX PS Example 3; SEQ ID NO 9; 34pp; English.

XX The present invention discloses a method of amplifying nucleic acid using  
XX primers and probes by rolling circle amplification method. The present  
XX invention comprises primer generation ? rolling circle amplification (PG-  
XX RCA) in which a ribbon probe is involved, allows the single step  
XX detection of nucleic acid sequences such as DNA and RNA sensitively and  
XX rapidly. This technology is easily applicable to detection of other  
XX biomolecules such as DNA methylation, single nucleotide polymorphism  
XX (SNP), protein and posttranslational modifications. PGR (primer  
XX generation reaction) is a reaction that is designed to produce at least  
XX one nucleic acid primer from a PGR initiation sequence of an RCR (rolling  
XX circle reaction) product and the resulting primer is designed to prime to  
XX a circular nucleic acid probe and initiate RCR. On the other hand, RCR is  
XX designed to produce concatenated sequence copies of the circular probe,  
XX in which the resulting product contains at least one PGR initiation  
XX sequence in every repeat sequence just like the initial reaction signal.  
XX The first and second nucleic acid primers are generated by one of  
XX nuclease-based cleavage reaction, strand displacement amplification,  
XX cleavage-initiated isothermal amplification, three-way junction  
XX isothermal amplification, three-way junction rolling circle reaction,  
XX binding assay using a nucleic acid labeled recognition agent and  
XX proximity assay. The method of nucleic acid detection using the present  
XX invention is useful for in vitro diagnostics and in pathogen detection.  
XX The nucleotide sequence presented here is the target nucleic acid for  
XX nuclease-based cleavage reaction PG-RCA.

SQ Sequence 24 BP; 5 A; 5 C; 6 G; 5 T; 3 U; 0 Other;

Query Match 85.0%; Score 17; DB 19; Length 24;  
Score over Length 70.8%;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGCCGT 20  
|||||  
Db 1 CCAGTTGAAGTTGCCGT 17

RESULT 154  
AEJ10484  
ID AEJ10484 standard; DNA; 24 BP.  
XX  
AC AEJ10484;  
XX  
DT 07-SEP-2006 (first entry)  
XX  
DE Target nucleic acid used in PG-RCA using ribbon probe.  
XX  
KW DNA detection; microorganism detection; SNP detection;  
KW epigenetic modification; diagnostic; RNA detection; DNA amplification;  
KW DNA methylation; gene amplification; primer extension; ss;  
KW DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_RNA 22..24  
FT /\*tag= a  
FT modified\_base 22..24  
FT /\*tag= b  
FT /\*mod\_base= 2'-O-methyluridine  
XX  
PN WO2006074162-A2.  
XX  
PD 13-JUL-2006.  
XX  
PF 04-JAN-2006; 2006WO-US000086.  
XX  
PR 04-JAN-2005; 2005US-0641255P.  
PR 14-JUL-2005; 2005US-0699340P.  
XX  
PA (HITB) HITACHI CHEM CO LTD.  
PA (HITB) HITACHI CHEM RES CENT INC.  
XX  
PI Murakami T;  
XX  
DR WPI; 2006-513365/52.  
XX  
PT Amplifying nucleic acid, by combining a nucleic acid primer with a  
PT polymerase and a circular nucleic acid probe, and producing a repeat of a  
PT sequence copy of the circular nucleic acid probe.  
XX  
PS Example 6; SEQ ID NO 16; 34pp; English.

The present invention discloses a method of amplifying nucleic acid using primers and probes by rolling circle amplification method. The present invention comprises primer generation, rolling circle amplification (PG-RCA) in which a ribbon probe is involved, allows the single step detection of nucleic acid sequences such as DNA and RNA sensitively and rapidly. This technology is easily applicable to detection of other biomolecules such as DNA methylation, single nucleotide polymorphism (SNP), protein and posttranslational modifications. PCR (primer generation reaction) is a reaction that is designed to produce at least one nucleic acid primer from a PCR initiation sequence of an RCR (rolling circle reaction) product and the resulting primer is designed to prime to a circular nucleic acid probe and initiate RCR. On the other hand, RCR is designed to produce concatenated sequence copies of the circular probe, in which the resulting product contains at least one PCR initiation sequence in every repeat sequence just like the initial reaction signal. The first and second nucleic acid primers are generated by one of nucleicase-based cleavage reaction, strand displacement amplification, cleavage-initiated isothermal amplification, three-way junction isothermal amplification, three-way junction rolling circle reaction, binding assay using a nucleic acid labeled recognition agent and

CC proximity assay. The method of nucleic acid detection using the present invention is useful for in vitro diagnostics and in pathogen detection. CC The nucleotide sequence presented here is the target nucleic acid used in PG-RCA using ribbon probe.  
XX  
SQ Sequence 24 BP; 5 A; 5 C; 6 G; 5 T; 3 U; 0 Other;  
Query Match 85.0%; Score 17; DB 19; Length 24;  
Score over Length 70.8%;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGCCGT 20  
|||||  
Db 1 CCAGTTGAAGTTGCCGT 17

RESULT 155  
ABS64186  
ID ABS64186 standard; DNA; 15 BP.  
XX  
AC ABS64186;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Tachykinin receptor gene TACR2, allele-specific probe #24.  
XX  
KW Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;  
KW tachykinin receptor.  
XX  
OS Homo sapiens.  
XX  
PN WO200263046-A1.  
XX  
PD 15-AUG-2002.  
XX  
PF 09-NOV-2001; 2001WO-US047394.  
XX  
PR 09-NOV-2000; 2000US-0247649P.  
XX  
PA (GENA-) GENAISANCE PHARM INC.  
XX  
PI Cappola G, Chew A, Gilson CR, Koshy B;  
XX  
DR WPI; 2002-636600/68.  
XX  
PT New genetic variants having polymorphisms in the Tachykinin receptor (TACR2) protein, useful for studying the function of TACR2, and for treating disorders associated with abnormal expression or function of TACR2 isogene.  
XX  
PS Claim 14; Page 14; 130pp; English.

The invention relates to an isolated polypeptide comprising a polymeric variant of a reference sequence for the Tachykinin receptor (TACR2) protein. Also described is a method for: (1) haplotyping or genotyping the TACR2 gene of an individual; (2) predicting a haplotype pair for the TACR2 gene of an individual; (3) identifying an association between a trait and at least one haplotype or haplotype pair of the TACR2 gene; and (4) isolated oligonucleotide for detecting a single nucleotide polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene are useful in studying the expression and biological function of TACR2, and in identifying drugs targeting TACR2 protein for treating disorders associated with abnormal expression or function of TACR2, e.g. asthma or breast cancer. Polynucleotides comprising a polymorphic gene variant or fragment may be used for therapeutic purposes, where a patient could benefit from expression or increased expression of a particular TACR2 protein isoform, or an expression vector encoding the isoform may be administered to the patient. Haplotype information is useful in improving the efficiency and output of several steps in drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. Information on polymorphisms may be applied in studying biological functions of TACR2 as well as in

CC identifying drugs targeting this protein for the treatment of disorders  
 CC related to its abnormal expression or function. ABS64163-ABS64302  
 CC represent human TACR2 gene allele-specific oligonucleotide probes and  
 CC primers used to detect haplotypes of the TACR2 gene of the invention  
 XX  
 SQ Sequence 15 BP; 3 A; 3 C; 4 G; 4 T; 0 U; 1 Other;

Query Match 53.0%; Score 10.6; DB 6; Length 15;  
 Score over Length 70.7%;  
 Best Local Similarity 90.9%; Pred. No. 3.8e+05;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
 ||||:|||||  
 Db 4 CCAGTTGAAGT 14

RESULT 156  
 AAX71130/c  
 ID AAX71130 standard; RNA; 17 BP.  
 XX AC  
 AC AAX71130;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Human KDR VEGF receptor hammerhead ribozyme substrate #142.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX  
 DR WPI; 1997-259017/23.  
 XX  
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 101; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 5 A; 3 C; 4 G; 4 T; 5 U; 0 Other;

Query Match 60.0%; Score 12; DB 2; Length 17;  
 Score over Length 70.6%;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCAGTTGAAGT 14  
 ||||:|||||  
 Db 17 CCAGTTGAAGT 6

RESULT 158  
 AEB61076/c  
 ID AEB61076 standard; mRNA; 17 BP.

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCAGTTGAAGT 14  
 ||||:|||||  
 Db 16 CCAGTTGAAGT 5

RESULT 157  
 AAX71129/c  
 ID AAX71129 standard; RNA; 17 BP.  
 XX AC  
 AC AAX71129;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Human KDR VEGF receptor hammerhead ribozyme substrate #141.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX  
 DR WPI; 1997-259017/23.  
 XX  
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 101; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 60.0%; Score 12; DB 2; Length 17;  
 Score over Length 70.6%;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+04;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCAGTTGAAGT 14  
 ||||:|||||  
 Db 17 CCAGTTGAAGT 6

RESULT 158  
 AEB61076/c  
 ID AEB61076 standard; mRNA; 17 BP.

XX AC AEB61076;  
XX DT 22-SEP-2005 (first entry)  
XX DE Human VEGF receptor 21 (Kdr) DNazyme target sequence SEQ ID 3654.  
XX KW VEGF receptor; angiogenesis; cancer; tumor; ocular disease;  
KW diabetic retinopathy; age related macular degeneration;  
KW angiogenesis disorder; rheumatoid arthritis; psoriasis; wound healing;  
KW endometriosis; endometrial carcinoma; gynecological bleeding disorder;  
KW menorrhagia disorder; premenstrual syndrome; menopause; Gynecological;  
KW Cystostatic; Ophthalmological; Antidiabetic; antitumor; Anticancer;  
KW Antipsoriatic; Antirheumatic; Antiarthritic; Vulnerary; Hemostatic;  
KW Contraceptive; ss; enzymatic nucleic acid.  
XX OS Homo sapiens.  
XX PN WO200296927-A2.  
XX PD 05-DEC-2002.  
XX PF 29-MAY-2002; 2002WO-US017674.  
XX PR 29-MAY-2001; 2001US-00870161.  
XX PR 30-NOV-2001; 2001US-0334461P.  
XX PR 03-MAY-2002; 2002US-00138674.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PA (CHIR-) CHIRON CORP.  
XX PI Escobedo J, Mcswiggen J, Pavco P, Stinchcomb D, Sandberg J;  
PI Gordon G;  
XX WPI; 2003-140439/13.  
XX DR Novel enzymatic nucleic acids, ribozymes, which modulate expression of  
XX PT genes encoding vascular endothelial growth factor and/or VEGF receptor,  
XX PT useful for inhibiting tumor angiogenesis in cell, and for treating  
XX PT cancer.  
XX PS Disclosure; SEQ ID NO 3654; 172pp; English.  
XX CC The invention relates to enzymatic nucleic acids (I) i.e.  
XX CC ribozymes/DNAzymes/Zinczymes that target and modulate expression of, genes  
XX CC encoding vascular endothelial growth factor (VEGF) and/or VEGF receptor  
XX CC (VEGFRI and 2 encode by the Flt-1 and Kdr genes respectively). Also  
XX CC included are a composition comprising (I) and a carrier, administering  
XX CC (I) to a cell (by contacting the cell with the compound under conditions  
XX CC suitable for the administration), administering (I) to a cell (in  
XX CC conjunction with one or more other drug by contacting the cell with the  
XX CC compound and the other drug under conditions suitable for the  
XX CC administration), administering (I) to a mammal (by contacting the mammal  
XX CC with the compound under conditions suitable for the administration),  
XX CC treating (M1) a subject having endometriosis (by contacting a subject  
XX CC with, or administering to subject, a nucleic acid molecule (II) that  
XX CC modulates expression of VEGF, VEGFR1, and/or VEGFR2), a mammalian cell  
XX CC (III) comprising (I) and administering to a mammal (I) (in conjunction  
XX CC with a chemotherapeutic agent comprising contacting the mammal with the  
XX CC compound and the chemotherapeutic agent under conditions suitable for the  
XX CC administration). (I) is administered to a mammalian cell, preferably  
XX CC human cell in the presence of a delivery reagent which is a lipid such as  
XX CC cationic lipid or phospholipid, or a liposome. The enzymatic nucleic acid  
XX CC molecule has an endonuclease activity to cleave RNA encoded by a VEGFR1  
XX CC or VEGFR2 gene, and is in a hammerhead, inozyme, DNazyme, G-cleaver,  
XX CC or Amberzyme configuration. The enzymatic nucleic acids are useful for  
XX CC inhibiting ocular angiogenesis associated with diabetic retinopathy or  
XX CC age-related diabetic retinopathy, in a subject. They are also useful for  
XX CC inhibiting angiogenesis, preferably tumor angiogenesis in cell, and for  
XX CC treating a subject having a condition associated with an increased level  
XX CC of VEGF receptor, where the condition is cancer, e.g. breast cancer, lung  
XX CC cancer (such as non-small cell lung carcinoma), colorectal cancer, renal  
XX CC cancer (such as renal cell carcinoma), pancreatic cancer. The enzymatic

CC nucleic acids are useful for treating a subject (preferably human) having  
CC endometriosis, psoriasis, age-related macular degeneration, proliferative  
CC diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis,  
CC wound healing, endometrial carcinoma, gynecologic bleeding disorders,  
CC irregular menstrual cycles, ovulation, premenstrual syndrome, and  
CC menopaual dysfunction. The enzymatic nucleic acids are useful for birth  
CC control by inhibiting ovulation or embryonic uterine implantation. The  
CC present sequence is a target sequence from the human VEGFR2/Kdr mRNA.  
XX SQ Sequence 17 BP; 5 A; 3 C; 4 G; 0 T; 5 U; 0 Other;  
Query Match 60.0%; Score 12; DB 8; Length 17;  
Score over length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 7.9e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 CCCAGTTGAAGT 14  
Db 14 CCCAGTTGAAGT 3  
RESULT 159  
AAT93676/C  
ID AAT93676 standard; DNA; 12 BP.  
XX AC AAT93676;  
XX DT 26-FEB-1998 (first entry)  
XX DE Exon-intron boundary of exon 8-9 of a mutant of the presenilin gene.  
XX KW Presenilin gene; PS-1 gene; early-onset Alzheimers disease; polymorphism;  
XX KW intron; splice site; diagnosis; beta-amyloid related disease;  
XX KW PS-1 isoforms; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT mutation 6  
XX FT /\*tag= a  
XX FT /note= "G replaced with T"  
XX PN EF785282-A2.  
XX PD 23-JUL-1997.  
XX PF 17-JAN-1997; 97EP-00300323.  
XX PR 19-JAN-1996; 96US-0010241P.  
XX PA (UNIW) UNIV WASHINGTON SCHOOL MED.  
XX PA (UYSP-) UNIV SOUTH FLORIDA.  
XX PA (SMIK) SMITHKLINE BEECHAM PLC.  
XX PI Goate AM, Hardy JA, Roberts GW;  
XX WPI; 1997-365951/34.  
XX DR Detection of presenilin-1 isoforms - used for the prognosis of head-  
XX PT injury subjects and the prognosis and treatment of beta-amyloid-related  
XX PT diseases.  
XX PS Example 3; Fig 1B; 26pp; English.  
XX CC The present sequence represents part of the DNA sequence from a novel  
XX CC splice mutant of the presenilin (PS-1) gene. Mutations in the PS-1 gene  
XX CC on chromosome 14 have been shown to cause a significant proportion of  
XX CC early-onset, autosomal dominant Alzheimers disease. Common polymorphisms  
XX CC within the intron 3' to exon 9 of the PS-1 gene were identified within  
XX CC and proximal to the intron. A mutation has been found in an early-onset  
XX CC Alzheimers disease designated F74. This mutation is in the last  
XX CC nucleotide of the intron between exons 8 and 9, where a G is replaced  
XX CC with a T. This mutation spoils the the acceptor site in the middle of





CC kappa genes inserted are selected to restore normal B-cell development in  
CC the mammal. The transgenic animals have a near complete human Ig locus,  
CC including both a human heavy chain locus and a human kappa light chain  
CC locus. They can be used for the production of human antibodies when  
CC exposed to particular antigens e.g. when exposed to human IL-8, EGFR or  
CC TNF- alpha the mice will produce antibodies to IL-8, EGFR or TNF- alpha  
CC respectively

XX  
SQ Sequence 12 BP; 2 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 2; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTG 10

|||||

12 GCCCCAGTAG 3

RESULT 162

ABH93674/C

ID ABH93674 standard; DNA; 12 BP.

XX AC ABH93674;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 293667 for detecting SNP TSC0015722.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 293667; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB12073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15

|||||

11 AGTTGAGATT 2

RESULT 163

ABI02985

ID ABI02985 standard; DNA; 12 BP.

XX AC ABI02985;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 302958 for detecting SNP TSC0020249.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 302958; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16

|||||

2 GTTGAAGATG 11

RESULT 164

ABI29616

ID ABI29616 standard; DNA; 12 BP.

XX



AC	ABI29616;
XX	
XX	22-FEB-2002 (first entry)
DE	22-FEB-2002 (first entry)
XX	Oligonucleotide primer SEQ ID NO 329589 for detecting SNP TSC0035020.
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
XX	
XX	WO200177384-A2.
XX	
XX	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
XX	07-APR-2000; 2000DE-01019173.
PR	
XX	(EPIG-) EPIGENOMICS AG.
PA	
XX	Olek A, Piepenbrock C, Berlin K;
PI	
XX	WPI; 2001-657177/75.
DR	
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single-nucleotide polymorphisms and cytosine
PT	methylation status.
PT	
XX	Claim 1; SEQ ID NO 329589; 29pp + Sequence Listing; German.
PS	
XX	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligonucleotides are also used for detecting cell type differentiation. ABC000010
CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC	represent the oligomers described in the invention. NOTE: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;
Query Match	42.0%; Score 8.4; DB 5; Length 12;
Score over Length	70.0%;
Best Local Similarity	90.0%; Pred. No. 4.4e+06;
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Oy	6 AGTTGAAGTT 15
Db	2 AGTTAAAGTT 11
RESULT 165	
ABI04904	
ID	ABI04904 standard; DNA; 12 BP.
XX	
AC	ABI04904;
XX	
XX	22-FEB-2002 (first entry)
XX	Oligonucleotide primer SEQ ID NO 304877 for detecting SNP TSC0021148.
DE	
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
OS	
XX	

EN	W0200177384-A2.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	
DR	WPI; 2001-657177/75.
XX	
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single-nucleotide polymorphisms and cytosine
PT	methylation status.
XX	
PS	Claim 1; SEQ ID NO 304877; 29pp + Sequence Listing; German.
XX	
CC	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligomers are also used for detecting cell type differentiation. ABC00010
CC	-ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC	represent the oligomers described in the invention. NOTE: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
Query Match	42.0%; Score 8.4; DB 5; Length 12;
Score over Length	70.0%;
Best Local Similarity	90.0%; Pred. No. 4.4e+06;
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	6 AGTTGAGTT 15
Db	2 AGTTGAGTT 11
RESULT 166	
ABH85666	
ID	ABH85666 standard; DNA; 12 BP.
XX	
AC	ABH85666;
XX	
DT	22-FEB-2002 (first entry)
XX	
DE	Oligonucleotide primer SEQ ID NO 285659 for detecting SNP TSC0012392.
XX	
KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
XX	
FN	W0200177384-A2.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	

DR WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 285659; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTT 15  
Db 1 AGTTGAGGTT 10  
RESULT 167  
ABI38969  
ID ABI38969 standard; DNA; 12 BP.  
XX  
AC ABI38969;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 338942 for detecting SNP TSC0040756.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 338942; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTT 15  
Db 1 AGTTGAGGTT 10  
RESULT 168  
ABH86874/C  
ID ABH86874 standard; DNA; 12 BP.  
XX  
AC ABH86874;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 286867 for detecting SNP TSC0012861.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 286867; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GTTGAAGTTG 16  
Db 1 GTTGAAGTAG 10

```
Score over Length      70.0%;
Best Local Similarity  90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 12 AGTTGAAGTT 3

RESULT 169
AB116132/c
ID AB116132 standard; DNA; 12 BP.
XX AC AB116132;
XX AC AB116132;
XX AC AB116132;
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 316105 for detecting SNP TSC0027285.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 316105; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1

RESULT 170
AB154959
ID AB154959 standard; DNA; 12 BP.

Score over Length      42.0%; Score 8.4; DB 5; Length 12;
Best Local Similarity  70.0%;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1

RESULT 171
AB143333
ID AB143333 standard; DNA; 12 BP.
XX AC AB143333;
XX AC AB143333;
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 343306 for detecting SNP TSC0010454.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
```

```
XX AB154959;
XX 22-FEB-2002 (first entry)
DT Oligonucleotide primer SEQ ID NO 354932 for detecting SNP TSC0010418.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 354932; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 1 GTTGAAGTTG 10

RESULT 171
AB143333
ID AB143333 standard; DNA; 12 BP.
XX AC AB143333;
XX AC AB143333;
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 343306 for detecting SNP TSC0010454.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
```

XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 343306; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GTTGAAGTTG 16  
DB ||| |||||  
3 GTTGAAGTTG 12  
RESULT 172  
ID ABH74215 standard; DNA; 12 BP.  
XX AC ABH74215;  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 274200 for detecting SNP TSC0003474.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
PI

XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 274200; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GTTGAAGTTG 16  
DB ||| |||||  
3 GTTGAAGTTG 12  
RESULT 173  
ID ABH17933/C  
XX AC ABH17933;  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 317906 for detecting SNP TSC028339.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 317906; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The

oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
| | | | |  
DB 12 AATTGAAGTT 3

RESULT 174  
ABH72571/c

ID ABH72571 standard; DNA; 12 BP.

XX ABH72571;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 272556 for detecting SNP TSC0002858.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 272556; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
| | | | |  
DB 12 AATTGAAGTT 3

RESULT 174  
ABH72571/c

ID ABH72571 standard; DNA; 12 BP.

XX ABH72571;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 272556 for detecting SNP TSC0002858.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 272556; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
| | | | |  
DB 11 AGTTTAAGTT 2

RESULT 175  
ABH81072

ID ABH81072 standard; DNA; 12 BP.

XX ABH81072;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 281065 for detecting SNP TSC0009391.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 281065; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
| | | | |  
DB 2 GTAGAAGTTG 11

RESULT 176  
ABI17272/c

```
ID  ABI17272 standard; DNA; 12 BP.
XX
AC  ABI17272;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 317245 for detecting SNP TSC0027885.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
DR  WPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 317245; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
    Query Match 42.0%; Score 8.4; DB 5; Length 12;
    Score over Length 70.0%;
    Best Local Similarity 90.0%; Pred. No. 4.4e+06;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  6 AGTTGAAGTT 15
DB  12 AGTTTAAGTT 3

RESULT 177
ABI28993/C
ID  ABI28993 standard; DNA; 12 BP.
XX
AC  ABI28993;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 328966 for detecting SNP TSC0034675.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
DR  WPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 317245; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
    Query Match 42.0%; Score 8.4; DB 5; Length 12;
    Score over Length 70.0%;
    Best Local Similarity 90.0%; Pred. No. 4.4e+06;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  6 AGTTGAAGTT 15
DB  12 AGTTTAAGTT 3

RESULT 178
ABI46836
ID  ABI46836 standard; DNA; 12 BP.
XX
AC  ABI46836;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 346809 for detecting SNP TSC0044779.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
```

PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 346809; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 2 AGTTGAAGAT 11  
RESULT 179  
ABH90231/C  
ID ABH90231 standard; DNA; 12 BP.  
XX  
AC ABH90231;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 290224 for detecting SNP TSC0014248.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PP 07-APR-2000; 2000DE-01019173.  
XX  
PR (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 290224; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 2 AGTTGAAGAT 11  
RESULT 179  
ABH90231/C  
ID ABH90231 standard; DNA; 12 BP.  
XX  
AC ABH90231;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 290224 for detecting SNP TSC0014248.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PP 07-APR-2000; 2000DE-01019173.  
XX  
PR (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 290224; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 2 AGTTGAAGAT 11  
RESULT 180  
ABI69058  
ID ABI69058 standard; DNA; 12 BP.  
XX  
AC ABI69058;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 369031 for detecting SNP TSC0057415.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PP 07-APR-2000; 2000DE-01019173.  
XX  
PR (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 369031; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

```
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 2 GGTGAAGTTG 11

RESULT 181
ABI59044/c
ID ABI59044 standard; DNA; 12 BP.
XX
AC ABI59044;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 359017 for detecting SNP TSC0051425.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 359017; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTTGAGTT 2

RESULT 182
ABI59044/c
ID ABI59044 standard; DNA; 12 BP.
XX
AC ABI59044;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 359017 for detecting SNP TSC0051425.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 359017; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTTGAGTT 2

RESULT 183
ABI27390/c
ID ABI27390 standard; DNA; 12 BP.
XX
AC ABI27390;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 327363 for detecting SNP TSC0033594.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```



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XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 327363; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC The range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 AGTTGAAGTT 15
Db 11 AGTTTAAGTT 2
RESULT 184
ABI31330/C
ID ABI31330 standard; DNA; 12 BP.
XX AC ABI31330;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 331303 for detecting SNP TSC0036110.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 316407; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC The range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 AGTTGAAGTT 15
Db 11 AGTTTAAGTT 2
RESULT 185
ABI16434
ID ABI16434 standard; DNA; 12 BP.
XX AC ABI16434;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 316407 for detecting SNP TSC0027431.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 316407; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC The range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GTTGAGTTG 16
Db 12 GTTGAGTTG 3
```

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
 Score over Length 70.0%;  
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GTTGAAGTTG 16  
 ||||| ||||  
 DB 1 GTTGAATTTG 10  
 ||||| ||||

RESULT 186  
 ABI06955  
 ID ABI06955 standard; DNA; 12 BP.  
 AC ABI06955;  
 XX  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 306928 for detecting SNP TSC0022250.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 PN 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 306928; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic  
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;  
 Query Match 42.0%; Score 8.4; DB 5; Length 12;  
 Score over Length 70.0%;  
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTT 15  
 ||||| ||||  
 DB 3 AGTTAAAGTT 12  
 ||||| ||||

RESULT 187  
 ABI63294  
 ID ABI63294 standard; DNA; 12 BP.  
 AC ABI63294;  
 XX  
 XX 22-FEB-2002 (first entry)  
 DT Oligonucleotide primer SEQ ID NO 363267 for detecting SNP TSC0053740.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 PN 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 363267; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic  
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;  
 Query Match 42.0%; Score 8.4; DB 5; Length 12;  
 Score over Length 70.0%;  
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTT 15  
 ||||| ||||  
 DB 2 AATTGAAGTT 11  
 ||||| ||||

```
RESULT 188
ABI75491/c
ID ABI75491 standard; DNA; 12 BP.
XX
XX AC ABI75491;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 375464 for detecting SNP TSC0061264.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF Oligonucleotide primer SEQ ID NO 375464 for detecting SNP TSC0061264.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 375464; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 AGTTGAAGTT 15
XX ||| |||||
XX DB 10 AGTGAAGTT 1
XX
XX RESULT 189
ABI66800/c
ID ABI66800 standard; DNA; 12 BP.
XX
XX AC ABI66800;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 366773 for detecting SNP TSC0055962.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 375464; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 AGTTGAAGTT 15
XX ||| |||||
XX DB 10 AGTGAAGTT 1
XX
XX RESULT 190
ABH80048/c
ID ABH80048 standard; DNA; 12 BP.
XX
XX AC ABH80048;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 280041 for detecting SNP TSC0080888.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX
```

PA (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX  
PS Claim 1; SEQ ID NO 280041; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 10 AGTTGAAGTT 1  
RESULT 191  
ABI92714/C  
ID ABH92714 standard; DNA; 12 BP.  
XX  
XX ABH92714;  
XX  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide primer SEQ ID NO 292707 for detecting SNP TSC0015313.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 292707; 29pp + Sequence Listing; German.  
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 2 C; 0 G; 5 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 10 AGTTGAAGTT 1  
RESULT 192  
ABI23882/C  
ID ABI23882 standard; DNA; 12 BP.  
XX  
XX ABI23882;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide primer SEQ ID NO 323855 for detecting SNP TSC0031647.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 323855; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX

```
XX SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 12 GTTGAGTTG 3

RESULT 193
AB116622/c
ID AB116622 standard; DNA; 12 BP.
XX AC AB116622;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 316595 for detecting SNP TSC0027519.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 316595; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 11 GTTGAATTG 2

RESULT 194
AB155037
ID AB155037 standard; DNA; 12 BP.
XX AC AB155037;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 355010 for detecting SNP TSC0049419.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 355010; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 3 AATTGAAGTT 12

RESULT 195
AB155337/c
ID AB155337 standard; DNA; 12 BP.
XX AC AB155337;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 355310 for detecting SNP TSC0049589.
XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX Central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 35310; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 GTTGAAGTTG 16  
Db 11 GTTGAAGTTG 2  
  
RESULT 196  
ABH72453  
ID ABH72453 standard; DNA; 12 BP.  
XX  
AC ABH72453;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 272438 for detecting SNP TSC0002817.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW Central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX Claim 1; SEQ ID NO 35310; 29pp + Sequence Listing; German.  
  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 GTTGAAGTTG 16  
Db 11 GTTGAAGTTG 2  
  
RESULT 197  
ABI33907  
ID ABI33907 standard; DNA; 12 BP.  
XX  
AC ABI33907;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 333880 for detecting SNP TSC0037804.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW Central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 333880; 29pp + Sequence Listing; German.

XX (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 272438; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 AGTTGAAGTT 15  
Db 3 AGTTGAAGTT 12  
  
RESULT 197  
ABI33907  
ID ABI33907 standard; DNA; 12 BP.  
XX  
AC ABI33907;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 333880 for detecting SNP TSC0037804.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW Central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 333880; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP),  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 3 AGTTGAAGTT 12

RESULT 198  
ABI76116  
ID ABI76116 standard; DNA; 12 BP.  
AC ABI76116;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 376089 for detecting SNP TSC0061604.  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 376089; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
DB 1 GTTGAAGTTG 10

RESULT 199  
ABI79656/C  
ID ABI79656 standard; DNA; 12 BP.  
XX  
XX AC ABI79656;  
XX  
XX DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 379629 for detecting SNP TSC0063392.  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 379629; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 10 AGTTGAAGTT 1

```

RESULT 200
ABH95097
ID ABH95097 standard; DNA; 12 BP.
XX
XX ABH95097;
AC
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide primer SEQ ID NO 295090 for detecting SNP TSC0016430.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX Oligonucleotide primer SEQ ID NO 274757 for detecting SNP TSC0003668.
DE
XX
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX Oligonucleotide primer SEQ ID NO 302312 for detecting SNP TSC0019928.
DE
XX
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTGAAGTTG 15
Db 10 AGTCGAAGTT 1

RESULT 202
ABH02339
ID ABH02339 standard; DNA; 12 BP.
XX
XX
AC ABH02339;
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide primer SEQ ID NO 302312 for detecting SNP TSC0019928.
DE
XX
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTGAAGTTG 15
Db 10 AGTCGAAGTT 1

RESULT 201
ABH74772/C
ID ABH74772 standard; DNA; 12 BP.
XX
XX
AC ABH74772;
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide primer SEQ ID NO 274757 for detecting SNP TSC0003668.
DE
XX
XX

```



```
PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 302312; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11
RESULT 203
ABI21522/c
ID ABI21522 standard; DNA; 12 BP.
XX
AC ABI21522;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 321495 for detecting SNP TSC0030284.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 302312; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11
RESULT 204
ABI06231/c
ID ABI06231 standard; DNA; 12 BP.
XX
AC ABI06231;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 306204 for detecting SNP TSC0021865.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 306204; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
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CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 2 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
   .| | | | | | |
   12 AATTGAAGTT 3

Db
RESULT 205
ABI10237
ID ABI10237 standard; DNA; 12 BP.
XX
AC ABI10237;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 310210 for detecting SNP TSC0023863.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 310210; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
   .| | | | | | |
   12 AATTGAAGTT 3

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 2 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
   .| | | | | | |
   12 AATTGAAGTT 3

Db
RESULT 206
ABI47132/C
ID ABI47132 standard; DNA; 12 BP.
XX
AC ABI47132;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 347105 for detecting SNP TSC0044912.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 347105; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 2 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
   .| | | | | | |
   11 AGTTAAGTT 2

Db
RESULT 207
ABH96302/C
ID ABH96302 standard; DNA; 12 BP.
XX
AC ABH96302;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 296295 for detecting SNP TSC0017012.
```

```
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX WO200177384-A2.
XX
PN 18-OCT-2001.
XX
PD 06-APR-2001; 2001WO-IB000713.
XX
PF 07-APR-2000; 2000DE-01019173.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 296295; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB ||| |||||
12 AGTAGAAGTT 3
RESULT 208
ABT08525
ID ABT06525 standard; DNA; 12 BP.
XX
AC ABT06525;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 306498 for detecting SNP TSC0022053.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX WO200177384-A2.
XX
PN 18-OCT-2001.
XX
PD 06-APR-2001; 2001WO-IB000713.
XX
PF 07-APR-2000; 2000DE-01019173.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
```

```
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 306498; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB ||| |||||
2 AGTTAAAGTT 11
RESULT 209
ABI31606/c
ID ABI31606 standard; DNA; 12 BP.
XX
AC ABI31606;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 331579 for detecting SNP TSC0036328.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX WO200177384-A2.
XX
PN 18-OCT-2001.
XX
PD 06-APR-2001; 2001WO-IB000713.
XX
PF 07-APR-2000; 2000DE-01019173.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
```

```
XX PS Claim 1; SEQ ID NO 331579; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAGTT 2

RESULT 210
ABI31734/c
ID ABI31734 standard; DNA; 12 BP.
XX AC ABI31734;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 331707 for detecting SNP TSC0036424.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 331707; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAGTT 2

RESULT 210
ABI31734/c
ID ABI31734 standard; DNA; 12 BP.
XX AC ABI31734;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 331707 for detecting SNP TSC0036424.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 331707; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 11 AGTTGAGTT 2

RESULT 211
ABI43151
ID ABI43151 standard; DNA; 12 BP.
XX AC ABI43151;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 343124 for detecting SNP TSC0042902.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 343124; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
```

```
Db      ||||| |||||
        2 AGTTAAGTT 11

RESULT 212
ABI36211/c
ID  ABI36211 standard; DNA; 12 BP.
XX
XX
AC  ABI36211;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 336184 for detecting SNP TSC0039238.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 336184; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
ftp.wipo.int/pub/published_pct_sequences
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTG 16
Db      ||||| |||||
        12 GTTGTAGTTG 3

RESULT 213
ABI59670
ID  ABI59670 standard; DNA; 12 BP.
XX
XX
AC  ABI59670;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 371399 for detecting SNP TSC0058753.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 336184; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
ftp.wipo.int/pub/published_pct_sequences
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      ||||| |||||
        1 AGTTGAGGTT 10

RESULT 214
ABI71426
ID  ABI71426 standard; DNA; 12 BP.
XX
XX
AC  ABI71426;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 371399 for detecting SNP TSC0058753.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
```



CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 AAGTGGCGT 20

Db 3 AAGTGTGCT 12

RESULT 217

ABH93128/c

ID ABH93128 standard; DNA; 12 BP.

XX AC ABH93128;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 293121 for detecting SNP TSC0015507.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 293121; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15

Db 12 AGTTGGAGTT 3

RESULT 218

ABH69605/c

ID ABH69605 standard; DNA; 12 BP.

XX AC ABH69605;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 269582 for detecting SNP TSC0001812.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 269582; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15

Db 10 AGTTGGAGTT 1

RESULT 219

ABI23801/c

ID ABI23801 standard; DNA; 12 BP.

XX AC ABI23801;

XX DT 22-FEB-2002 (first entry)

```
XX DE Oligonucleotide primer SEQ ID NO 323774 for detecting SNP TSC0031607.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 323774; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIO0010-ABIO2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTT 15
XX DB | | | | | | |
XX 12 ATTGAAGTT 3
XX RESULT 220
XX ABH70890/C
XX ID ABH70890 standard; DNA; 12 BP.
XX AC ABH70890;
XX XX 22-FEB-2002 (first entry)
XX DT
XX DE Oligonucleotide primer SEQ ID NO 270867 for detecting SNP TSC0035126.
XX XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 270867; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIO0010-ABIO2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTT 15
XX DB | | | | | | |
XX 12 ATTGAAGTT 3
XX RESULT 221
XX ABH70890
XX ID ABH70890 standard; DNA; 12 BP.
XX AC ABH70890;
XX XX 22-FEB-2002 (first entry)
XX DT
XX DE Oligonucleotide primer SEQ ID NO 329753 for detecting SNP TSC0035126.
XX XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 270867; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABIO0010-ABIO2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 6 AGTTGAAGTT 15
XX DB | | | | | | |
XX 10 AGTTGAAGTT 1
```



PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX  
XX  
PS Claim 1; SEQ ID NO 329753; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
|||||  
Db 3 GTTGAAGTTG 12

RESULT 222  
ABI12820

ID ABI12820 standard; DNA; 12 BP.

AC ABI12820;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 312793 for detecting SNP TSC0025301.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 312793; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
|||||  
Db 2 GTTGAAGTTG 11

RESULT 223

ABI47302

ID ABI47302 standard; DNA; 12 BP.

XX

AC ABI47302;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 347275 for detecting SNP TSC0045008.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 347275; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 12 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;





CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTT 15  
|||||  
DB 3 AGTTGAAGTT 12  
|||||

RESULT 229  
ABH81937/c  
ID ABH81937 standard; DNA; 12 BP.

XX AC ABH81937;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 281930 for detecting SNP TSC0010165.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
XX PT methylation status.

XX PS Claim 1; SEQ ID NO 281930; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 7 GTTGAAGTTG 16  
|||||  
DB 11 GTTGTAGTTG 2  
|||||

RESULT 230

ABI73613  
ID ABI73613 standard; DNA; 12 BP.

XX AC ABI73613;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 373586 for detecting SNP TSC0060183.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
XX PT methylation status.

XX PS Claim 1; SEQ ID NO 373586; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGTTGAAGTT 15  
|||||

DB 1 AGTTGTAGTT 10  
|||||

RESULT 231

ABI53913/c

ID ABI53913 standard; DNA; 12 BP.

XX AC ABI53913;

```
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 353886 for detecting SNP TSC0048785.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 300438; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
    Query Match 42.0%; Score 8.4; DB 5; Length 12;
    Score over Length 70.0%;
    Best Local Similarity 90.0%; Pred. No. 4.4e+06;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 12 AGTTGAAGAT 3
RESULT 232
AB100465
ID AB100465 standard; DNA; 12 BP.
XX AC AB100465;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 300438 for detecting SNP TSC0019035.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 353886; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
    Query Match 42.0%; Score 8.4; DB 5; Length 12;
    Score over Length 70.0%;
    Best Local Similarity 90.0%; Pred. No. 4.4e+06;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 12 AGTTGAAGAT 3
RESULT 232
AB100465
ID AB100465 standard; DNA; 12 BP.
XX AC AB100465;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 299239 for detecting SNP TSC0018492.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 299239 for detecting SNP TSC0018492.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 299239 for detecting SNP TSC0018492.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
```

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 299239; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 3 ATTTGAAGTT 12

RESULT 234  
ABH88414/c  
ID ABH88414 standard; DNA; 12 BP.  
XX  
AC ABH88414;  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 288407 for detecting SNP TSC0013497.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 288407; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
DB 12 GTTAAAGTTG 3

RESULT 235  
ABI66132/c  
ID ABI66132 standard; DNA; 12 BP.  
XX  
AC ABI66132;  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 366105 for detecting SNP TSC0010825.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 366105; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;

```
Best Local Similarity 90.0%; Pred. No. 4.4e+06; Mismatches 0; Indels 1; Gaps 0;
Matches 9; Conservative 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTGAAGTT 2

RESULT 236
ABI67005/c
ID ABI67005 standard; DNA; 12 BP.
XX AC ABI67005;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 366978 for detecting SNP TSC0056077.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 366978; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GTTGAAGTTG 3

RESULT 237
ABI67274
ID ABI67274 standard; DNA; 12 BP.
XX AC ABI67274;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352722 for detecting SNP TSC0048058.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 367247; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 1 AGTGAAGTT 10

RESULT 238
ABI52749
ID ABI52749 standard; DNA; 12 BP.
XX AC ABI52749;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352722 for detecting SNP TSC0048058.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 367247; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

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PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 316596; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 7 GTTGAAGTTG 16
Db 2 GTTGAAGTTG 11
RESULT 239
AB116623/C
ID AB116623 standard; DNA; 12 BP.
XX
AC AB116623;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 316596 for detecting SNP TSC0027519.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 352722; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 7 GTTGAAGTTG 16
Db 2 GTTGAAGTTG 11
RESULT 240
AB144330
ID AB144330 standard; DNA; 12 BP.
XX
AC AB144330;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 344303 for detecting SNP TSC0043488.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 344303; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 7 GTTGAAGTTG 16
Db 11 GTTGAAGTTG 2
RESULT 240
AB144330
ID AB144330 standard; DNA; 12 BP.
XX
AC AB144330;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 344303 for detecting SNP TSC0043488.
XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 344303; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 7 GTTGAAGTTG 16
Db 11 GTTGAAGTTG 2

```



CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 2 AGTTGAAGTT 11

## RESULT 241

ABI61490  
ID ABI61490 standard; DNA; 12 BP.

XX  
AC ABI61490;

XX  
DT 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 361463 for detecting SNP TSC0052647.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX  
FN WO200177384-A2.

XX  
PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 361463; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;

Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 3 AGTTGAAGTT 12

## RESULT 242

ABI74887  
ID ABI74887 standard; DNA; 12 BP.

XX  
AC ABI74887;

XX  
DT 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 374860 for detecting SNP TSC0060940.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX  
FN WO200177384-A2.

XX  
PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 374860; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
|||||  
Db 2 GTTGAAGTTG 11

## RESULT 243

ABI10236  
ID ABI10236 standard; DNA; 12 BP.

```
XX AC ABI10236;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 310209 for detecting SNP TSC0023863.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 310209; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db 1 GTTGAAGTTG 10
RESULT 244
ABI1459/C
ID ABI1459 standard; DNA; 12 BP.
XX AC ABI1459;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 31432 for detecting SNP TSC0036202.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
```

```
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 31432; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;
XX Score over Length 70.0%;
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db 12 GTTGAAGTTG 3
RESULT 245
ABI32242/C
ID ABI32242 standard; DNA; 12 BP.
XX AC ABI32242;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 332215 for detecting SNP TSC0036773.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
```

XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
XX PT methylation status.  
XX PS Claim 1; SEQ ID NO 332215; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ . Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 11 AGTTGAAGTT 2  
RESULT 246  
ABI69897  
ID ABI69897 standard; DNA; 12 BP.  
XX AC ABI69897;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 369870 for detecting SNP TSC0057857.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
XX PT methylation status.  
XX PS Claim 1; SEQ ID NO 369870; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ . Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 11 AGTTGAAGTT 2  
RESULT 246  
ABI69897  
ID ABI69897 standard; DNA; 12 BP.  
XX AC ABI69897;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 369870 for detecting SNP TSC0057857.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
XX PT methylation status.  
XX PS Claim 1; SEQ ID NO 369870; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ . Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
DB 1 AGTTGAAGTT 10  
RESULT 247  
ABH92665/c  
ID ABH92665 standard; DNA; 12 BP.  
XX AC ABH92665;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 292658 for detecting SNP TSC0015297.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
XX PT methylation status.  
XX PS Claim 1; SEQ ID NO 292658; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ . Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

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Query Match      42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
DB      11 AGTTGAAGAT 2

RESULT 248
ABI29165/c
ID ABI29165 standard; DNA; 12 BP.
XX
AC ABI29165;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 329138 for detecting SNP TSC0034774.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 329138 for detecting SNP TSC0034774.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DT 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 329138; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
Query Match      42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
DB      10 AGTTGAAGTT 1

RESULT 249
ABI22105/c
ID ABI22105 standard; DNA; 12 BP.
XX
AC ABI22105;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 322078 for detecting SNP TSC0030647.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DT 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 322078; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match      42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
DB      10 AGTTGAAGTT 1

RESULT 250
ABH97330
ID ABH97330 standard; DNA; 12 BP.
XX
AC ABH97330;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 297323 for detecting SNP TSC0017523.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```

```
OS Homo sapiens.
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 297323; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB ||||| |||||
2 AGTTGTAAGTT 11
RESULT 251
ABI02630/C
ID ABI02630 standard; DNA; 12 BP.
XX
AC ABI02630;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 302603 for detecting SNP TSC0020078.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 297323; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB ||||| |||||
2 AGTTGTAAGTT 11
RESULT 252
ABH84497
ID ABH84497 standard; DNA; 12 BP.
XX
AC ABH84497;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 284490 for detecting SNP TSC0011855.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 284490; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
```

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
Db 2 AGTGAAGTT 11

RESULT 253  
ABI38801/c  
ID ABI38801 standard; DNA; 12 BP.

XX ABI38801;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 338774 for detecting SNP TSC0040669.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 338774; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
Db 10 ATTTGAAGTT 1

RESULT 254  
ABI62796/c  
ID ABI62796 standard; DNA; 12 BP.

XX ABI62796;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 362769 for detecting SNP TSC0053437.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 362769; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
Db 10 AGATGAAGTT 1

RESULT 255

```
AB164102
ID ABI64102 standard; DNA; 12 BP.
XX
XX
AC ABI64102;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide primer SEQ ID NO 364075 for detecting SNP TSC0054253.
XX
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX
OS Homo sapiens.
XX
XX
FN WO200177384-A2.
XX
XX
PD 18-OCT-2001.
XX
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX
PA (EPIC-) EPIGENOMICS AG.
XX
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX
WPI; 2001-657177/75.
XX
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
PS Claim 1; SEQ ID NO 364075; 29pp + Sequence Listing; German.
XX
XX
PA (EPIC-) EPIGENOMICS AG.
XX
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX
WPI; 2001-657177/75.
XX
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
PS Claim 1; SEQ ID NO 364075; 29pp + Sequence Listing; German.
XX
XX
PA This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
QY 6 AGTTGAGTT 15
Db |||||
1 AGTTGAGTT 10
XX
XX
RESULT 256
ABH92662/c
ID ABH92662 standard; DNA; 12 BP.
XX
XX
AC ABH92662;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide primer SEQ ID NO 292655 for detecting SNP TSC0015296.
XX
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX
OS Homo sapiens.
XX
XX
FN WO200177384-A2.
XX
XX
PD 18-OCT-2001.
XX
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX
PA (EPIC-) EPIGENOMICS AG.
XX
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX
WPI; 2001-657177/75.
XX
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
PS Claim 1; SEQ ID NO 292655; 29pp + Sequence Listing; German.
XX
XX
PA This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
QY 6 AGTTGAGTT 15
Db |||||
1 AGTTGAGTT 10
XX
XX
RESULT 257
ABI18502/c
ID ABI18502 standard; DNA; 12 BP.
XX
XX
AC ABI18502;
XX
XX
DT 22-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide primer SEQ ID NO 318475 for detecting SNP TSC0028677.
XX
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX
OS Homo sapiens.
XX
XX
FN WO200177384-A2.
XX
XX
PD 18-OCT-2001.
XX
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX
PA (EPIC-) EPIGENOMICS AG.
```

XX Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 318475; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
Db 10 AGTTGAAGTT 1  
RESULT 258  
ABI47133/C  
ID ABI47133 standard; DNA; 12 BP.  
XX  
XX  
AC ABI47133;  
XX  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 347106 for detecting SNP TSC0044912.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 347106; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 2 C; 1 G; 5 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTT 15  
Db 11 AGTTGAAGTT 2  
RESULT 259  
ABI4721/C  
ID ABI4721 standard; DNA; 12 BP.  
XX  
XX  
AC ABI4721;  
XX  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 341694 for detecting SNP TSC0042185.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 341694; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX



```
SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
  Query Match      42.0%; Score 8.4; DB 5; Length 12;
  Score over Length 70.0%;
  Best Local Similarity 90.0%; Pred. No. 4.4e+06;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
Db 10 GTTGAGGTG 1

RESULT 260
ABI42212/c
ID ABI42212 standard; DNA; 12 BP.
XX AC ABI42212;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 342185 for detecting SNP TSC0042419.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PN WO200177384-A2.
XX DR 18-OCT-2001.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 342185; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
  Query Match      42.0%; Score 8.4; DB 5; Length 12;
  Score over Length 70.0%;
  Best Local Similarity 90.0%; Pred. No. 4.4e+06;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
Db 11 AGTTAAAGTT 2

RESULT 262
ABI67350/c
ID ABI67350 standard; DNA; 12 BP.
XX AC ABI67350;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 367323 for detecting SNP TSC0009154.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX Claim 1; SEQ ID NO 367323; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI92073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;  
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;  
XX Score over Length 70.0%;  
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX 6 AGTTGAAGTT 15  
XX 10 AGTTAAAGTT 1  
XX  
XX RESULT 263  
XX ID ABI80116 standard; DNA; 12 BP.  
XX AC ABI80116;  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 380089 for detecting SNP TSC0063628.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX Claim 1; SEQ ID NO 269967; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI92073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;  
XX Query Match 42.0%; Score 8.4; DB 5; Length 12;  
XX Score over Length 70.0%;  
XX Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX 6 AGTTGAAGTT 15  
XX 1 AGTTAAAGTT 10  
XX  
XX RESULT 264  
XX ID ABH69990/C  
XX AC ABH69990;  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 269967 for detecting SNP TSC0001948.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX Claim 1; SEQ ID NO 269967; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

QY Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 6 AGTTGAAGTT 15  
11 AGTTGAAGAT 2

RESULT 265  
ABH95291  
ID ABH95291 standard; DNA; 12 BP.  
AC ABH95291;  
XX  
DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 295284 for detecting SNP TSC0016521.  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX  
PS Claim 1; SEQ ID NO 295284; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

QY Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 6 AGTTGAAGTT 15  
3 AGTTGAAGTT 12

RESULT 266  
ABH98049  
ID ABH98049 standard; DNA; 12 BP.  
XX  
AC ABH98049;  
XX  
DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 298042 for detecting SNP TSC0017887.  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX  
PS Claim 1; SEQ ID NO 298042; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

QY Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 7 GTTGAAGTTG 16  
3 GTGGAAGTTG 12

```
RESULT 267
ABI33882/c
ID ABI33882 standard; DNA; 12 BP.
XX
AC ABI33882;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 333855 for detecting SNP TSC0037792.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 333855; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABIO0010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGTTGAAGTT 15
DB 11 AGTTGAAGTT 2
XX
RESULT 268
ABI41817/c
ID ABI41817 standard; DNA; 12 BP.
XX
AC ABI41817;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 341790 for detecting SNP TSC0042229.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 341790; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABIO0010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GTTGAAGTTG 16
DB 12 GTTGAAGTTG 3
XX
RESULT 269
ABI48505/c
ID ABI48505 standard; DNA; 12 BP.
XX
AC ABI48505;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 348478 for detecting SNP TSC0045610.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
```

```
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 348478; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 ATTGAAGTT 2
|||||
11 AGTTGAAGTT 2

RESULT 270
ABI76925/c
ID ABI76925 standard; DNA; 12 BP.
XX AC ABI76925;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 376898 for detecting SNP TSC0062033.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 376898; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 4.4e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTTGAAGTT 2
|||||
11 AGTTGAAGTT 2

RESULT 271
ABI72013
ID ABI72013 standard; DNA; 12 BP.
XX AC ABI72013;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 371986 for detecting SNP TSC0059100.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 371986; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
```



KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX WO200177384-A2.  
XX  
XX  
PD 18-OCT-2001.  
XX  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX  
DR WPI; 2001-657177/75.  
XX  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX  
PS Claim 1; SEQ ID NO 364597; 29pp + Sequence Listing; German.  
XX  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 7 GTTGAAGTTG 16  
Db 12 GATGAAGTTG 3  
RESULT 275  
ABI62006/C  
ID ABI62006 standard; DNA; 12 BP.  
AC  
AC ABI62006;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 361979 for detecting SNP TSC0052975.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX  
PN WO200177384-A2.  
XX  
XX  
PD 18-OCT-2001.  
XX  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX

PR 07-APR-2000; 2000DE-01019173.  
XX  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX  
DR WPI; 2001-657177/75.  
XX  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX  
PS Claim 1; SEQ ID NO 361979; 29pp + Sequence Listing; German.  
XX  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 6 AGTTGAAGTT 15  
Db 12 AGTTGAAGTT 3  
RESULT 276  
ABI17895/C  
ID ABI17895 standard; DNA; 12 BP.  
XX  
AC ABI17895;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 317868 for detecting SNP TSC0028311.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX  
PN WO200177384-A2.  
XX  
XX  
PD 18-OCT-2001.  
XX  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX  
DR WPI; 2001-657177/75.  
XX  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX

PS Claim 1; SEQ ID NO 317868; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 11 ATTGAAGTT 2

RESULT 277  
ABH94593/C  
ID ABH94593 standard; DNA; 12 BP.

XX ABH94593;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 294586 for detecting SNP TSC0016192.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPTG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is PT designed to detect single-nucleotide polymorphisms and cytosine PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 294586; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 11 ATTGAAGTT 2

RESULT 277  
ABH94593/C  
ID ABH94593 standard; DNA; 12 BP.

XX ABH94593;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 294586 for detecting SNP TSC0016192.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPTG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is PT designed to detect single-nucleotide polymorphisms and cytosine PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 294586; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 11 ATTGAAGTT 2

RESULT 278  
ABH96494  
ID ABH96494 standard; DNA; 12 BP.

XX ABH96494;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 296487 for detecting SNP TSC0017101.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is PT designed to detect single-nucleotide polymorphisms and cytosine PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 296487; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 5; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 11 ATTGAAGTT 2





XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIC-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 347597; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 42.0%; Score 8.4; DB 5; Length 12;  
 Score over Length 70.0%;  
 Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 7 GTTGAATTG 16  
 Db 11 GTTGAATTG 2  
 RESULT 282  
 ABI77409/C  
 ID ABI77409 standard; DNA; 12 BP.  
 XX AC ABI77409;  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide primer SEQ ID NO 377382 for detecting SNP TSC0062298.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIC-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 377382; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 42.0%; Score 8.4; DB 5; Length 12;  
 Score over Length 70.0%;  
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 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 6 AGTTGAAGTT 15  
 Db 11 AATTGAAGTT 2  
 RESULT 283  
 ADD69888/C  
 ID ADD69888 standard; DNA; 12 BP.  
 XX AC ADD69888;  
 XX 15-JAN-2004 (first entry)  
 XX Let-7 L6 loop DNA.  
 XX down-regulation; RNA degradation; toxic protein knock-down;  
 KW virus production; GL2; Let-7; GL3; ds.  
 XX Unidentified.  
 XX WO2003020931-A2.  
 XX 13-MAR-2003.  
 XX 29-AUG-2002; 2002WO-EP009670.  
 XX 01-SEP-2001; 2001US-0317229P.  
 XX 04-JUN-2002; 2002US-0385733P.  
 XX (GALA-) GALAPAGOS GENOMICS NV.  
 XX Arts G, Langemeijer EV, Piest I, Van Es HHG, Michiels GAM;  
 XX WPI; 2003-290193/28.  
 XX Novel polynucleotide useful for down regulation or degradation of  
 PT specific RNA molecule in host cell, has sequence complementary to host  
 PT RNA sequence and linked to a sequence capable of forming stem-loop  
 PT structure.  
 XX Example 2; Fig 11; 166pp; English.  
 XX The invention relates to a novel isolated polynucleotide useful for the  
 CC down-regulation or degradation of a specific RNA molecule in a host cell  
 CC comprising a first polynucleotide sequence complementary to the RNA  
 CC sequence in the host cell, covalently linked to a second RNA sequence  
 CC capable of forming a stem-loop structure where the first polynucleotide  
 CC is an RNA sequence or a single-stranded DNA equivalent. The  
 CC polynucleotide of the invention may be useful for the down regulation or  
 CC degradation of a specific RNA molecule in a host cell, for producing

CC viral vectors encoding a toxic protein, for treatment in a human or  
CC animal and for temporary knock-down of proteins, such as lethal proteins,  
CC during virus production. The current sequence is that of the Let-7 loop  
CC DNA of the invention.

XX SQ Sequence 12 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 42.0%; Score 8.4; DB 8; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAA 12  
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Db 10 CCCAGTTCAA 1

RESULT 284  
AER38463/c  
ID AER38463 standard; DNA; 12 BP.

XX AER38463;

XX 05-APR-2007 (first entry)

XX Lipid metabolism protein (LMP) related DNA SEQ ID NO:132.

XX Genetic engineering; plant growth regulation; gene expression; seed;  
XX lipid metabolism protein; LMP; transgenic plant; oil; drought tolerance;  
XX cold tolerance; plant; ds.

OS Synthetic.  
OS Unidentified.

XX WO2007012576-A2.

XX 01-FEB-2007.

XX 14-JUL-2006; 2006WO-EP064276.

XX 25-JUL-2005; 2005US-0595649P.

XX (BADI ) BASF PLANT SCI.

XX Zank T, Oswald O;

XX WPI; 2007-176883/17.

XX New isolated lipid metabolism protein polynucleotides and polypeptides,  
PT useful for stimulating or modulating plant growth and plant yield, e.g.  
PT increasing plant growth under adverse conditions of drought, cold, or  
PT light.

PS Claim 6; SEQ ID NO 132; 128pp; English.

XX The invention relates to an isolated nucleic acid comprising two or more  
CC lipid metabolism protein (LMP) polynucleotide sequences encoding LMP  
CC polypeptides. The invention also relates to an expression vector  
CC containing the nucleic acid, where the nucleic acid is operatively linked  
CC to a promoter selected from a seed-specific promoter, a root-specific  
CC promoter or a non-tissue-specific promoter, a method of producing a  
CC transgenic plant having a modified level of a seed storage compound  
CC weight percentage compared to an empty vector control, a method of  
CC modulating the level of a seed storage compound weight percentage in a  
CC plant comprising modifying the expression of a nucleic acid in the plant,  
CC a transgenic plant made by the method and a seed produced by the  
CC transgenic plant, where the plant expresses the polypeptide that  
CC functions as a modulator of a seed storage compound and where the plant  
CC is true breeding for a modified level of seed storage compound weight  
CC percentage as compared to an empty vector control. The polynucleotides  
CC and polypeptides are useful for producing transgenic plants with improved  
CC quality traits, for manipulating fatty acid-related compounds, for  
CC increasing oil levels and for altering the fatty acid composition in

CC plants and seeds. The sequences are also useful for stimulating or  
CC modulating plant growth and plant yield, preferably for increasing plant  
CC growth under adverse conditions (e.g. drought, cold, light, UV) and for  
CC improving seed germination and seed dormancy, thus improving plant growth  
CC and/or yield of seed storage compounds. This sequence represents LMP  
CC related DNA of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 12 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 2 Other;

Query Match 42.0%; Score 8.4; DB 22; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 75.0%; Pred. No. 4.4e+06;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17  
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Db 12 AGYTGASGTGGC 1

Search completed: December 4, 2007, 01:29:56  
Job time : 474 secs

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 17:15:22 ; Search time 17683 seconds  
(without alignments)  
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Title: US-10-728-509-64

Perfect score: 20

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 93186685 seqs, 32758818645 residues

Total number of hits satisfying chosen parameters: 1276

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Listing first 1000 summaries

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48	12	85.7	60.0	14	3	PCT-US07-68404-1552	Sequence 1	C 121	9.4	78.3	47.0	12	40	US-10-257-017B-345090	Sequence 3
49	12	85.7	60.0	14	3	PCT-US07-68406-1552	Sequence 1	C 122	9.4	78.3	47.0	12	40	US-10-257-017B-361423	Sequence 3
50	12	85.7	60.0	14	3	PCT-US07-68408-1552	Sequence 1	C 123	9.4	78.3	47.0	12	51	US-10-708-952A-226611	Sequence 2
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53	12	85.7	60.0	14	81	PCT-US02-22417-5	Sequence 5	C 126	9.4	78.3	47.0	12	52	US-10-708-953-425654	Sequence 4
54	15	83.3	75.0	18	1	US-09-908-147-5	Sequence 5	C 127	9.4	78.3	47.0	12	52	US-10-708-953-675075	Sequence 6
55	15	83.3	75.0	18	34	US-10-728-509-5	Sequence 5	C 128	9.4	78.3	47.0	12	52	US-10-708-953-820071	Sequence 8
56	15	83.3	75.0	18	56	US-10-257-017B-271773	Sequence 2	C 129	9.4	78.3	47.0	12	52	US-10-708-953-1049802	Sequence 1
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58	10	83.3	50.0	12	40	US-10-257-017B-310208	Sequence 3	C 131	9.4	78.3	47.0	12	52	US-10-708-953-1160477	Sequence 1
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62	10	83.3	50.0	12	40	PCT-US02-22417-119	Sequence 1	C 135	9.4	78.3	47.0	12	52	US-10-708-953-2110468	Sequence 2
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83	11.4	81.4	57.0	14	60	US-10-594-448-16	Sequence 1	C 156	12.4	77.5	62.0	16	40	US-10-227-565-54229	Sequence 5
84	16	80.0	60.0	20	48	US-09-708-690-4126	Sequence 4	C 157	12.4	77.5	62.0	16	46	US-10-367-832A-54229	Sequence 5
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C 159	10.8	77.1	54.0	14	52	US-10-708-953-528084	Sequence 5	232	9.8	75.4	49.0	13	52	US-10-708-953-1014267	Sequence 1
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C 164	10.8	77.1	54.0	14	52	US-10-708-953-1713144	Sequence 1	C 237	9.8	75.4	49.0	13	52	US-10-708-953-1618678	Sequence 1
C 165	10.8	77.1	54.0	14	52	US-10-708-953-1883139	Sequence 1	C 238	9.8	75.4	49.0	13	52	US-10-708-953-1873083	Sequence 1
C 166	10.8	77.1	54.0	14	52	US-10-708-953-1898598	Sequence 1	C 239	9.8	75.4	49.0	13	52	US-10-708-953-2013164	Sequence 2
C 167	10.8	77.1	54.0	14	52	US-10-708-953-2077386	Sequence 2	C 240	9.8	75.4	49.0	13	52	US-10-708-953-2083562	Sequence 2
C 168	10.8	77.1	54.0	14	53	US-10-708-953A-528084	Sequence 5	C 241	9.8	75.4	49.0	13	52	US-10-708-953-2156300	Sequence 2
C 169	10.8	77.1	54.0	14	53	US-10-708-953A-613923	Sequence 6	C 242	9.8	75.4	49.0	13	52	US-10-708-953-2181596	Sequence 2
C 170	10.8	77.1	54.0	14	53	US-10-708-953A-668724	Sequence 6	C 243	9.8	75.4	49.0	13	53	US-10-708-953A-519962	Sequence 5
C 171	10.8	77.1	54.0	14	53	US-10-708-953A-1269719	Sequence 1	C 244	9.8	75.4	49.0	13	53	US-10-708-953A-683001	Sequence 6
C 172	10.8	77.1	54.0	14	53	US-10-708-953A-1475347	Sequence 1	C 245	9.8	75.4	49.0	13	53	US-10-708-953A-755878	Sequence 7
C 173	10.8	77.1	54.0	14	53	US-10-708-953A-1713144	Sequence 1	C 246	9.8	75.4	49.0	13	53	US-10-708-953A-804357	Sequence 8
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C 182	10.8	76.9	50.0	13	24	US-10-051-645B-5965	Sequence 5	C 255	9.8	75.4	49.0	13	53	US-10-708-953A-2013164	Sequence 2
C 183	10.8	76.9	50.0	13	38	US-10-257-017B-28743	Sequence 2	C 256	9.8	75.4	49.0	13	53	US-10-708-953A-2083562	Sequence 2
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C 197	10.8	76.9	50.0	13	40	US-10-257-017B-171652	Sequence 1	C 270	9.75	45.0	45.0	12	40	US-10-257-017B-272526	Sequence 2
C 198	10.8	76.9	50.0	13	62	US-11-043-842-704	Sequence 7	C 271	9.75	45.0	45.0	12	40	US-10-257-017B-281370	Sequence 2
C 199	10.8	76.9	50.0	13	62	US-11-051-720-809	Sequence 8	C 272	9.75	45.0	45.0	12	40	US-10-257-017B-284630	Sequence 2
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C 201	11.4	76.0	57.0	15	1	PCT-US02-25943-11543	Sequence 1	C 274	9.75	45.0	45.0	12	40	US-10-257-017B-298602	Sequence 2
C 202	11.4	76.0	57.0	15	40	US-10-257-565-11543	Sequence 1	C 275	9.75	45.0	45.0	12	40	US-10-257-017B-298745	Sequence 2
C 203	11.4	76.0	57.0	15	41	US-10-299-054A-10916	Sequence 1	C 276	9.75	45.0	45.0	12	40	US-10-257-017B-299931	Sequence 2
C 204	11.4	76.0	57.0	15	46	US-10-367-832A-11543	Sequence 1	C 277	9.75	45.0	45.0	12	40	US-10-257-017B-303341	Sequence 2
C 205	11.4	76.0	57.0	15	52	US-10-708-953-383591	Sequence 3	C 278	9.75	45.0	45.0	12	40	US-10-257-017B-305026	Sequence 3
C 206	11.4	76.0	57.0	15	52	US-10-708-953-409578	Sequence 4	C 279	9.75	45.0	45.0	12	40	US-10-257-017B-307994	Sequence 3
C 207	11.4	76.0	57.0	15	52	US-10-708-953-572403	Sequence 5	C 280	9.75	45.0	45.0	12	40	US-10-257-017B-310012	Sequence 3
C 208	11.4	76.0	57.0	15	52	US-10-708-953-716806	Sequence 7	C 281	9.75	45.0	45.0	12	40	US-10-257-017B-319646	Sequence 3
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C 210	11.4	76.0	57.0	15	52	US-10-708-953-1276947	Sequence 1	C 283	9.75	45.0	45.0	12	40	US-10-257-017B-333972	Sequence 3
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C 213	11.4	76.0	57.0	15	53	US-10-708-953A-409578	Sequence 4	C 286	9.75	45.0	45.0	12	40	US-10-257-017B-360215	Sequence 3
C 214	11.4	76.0	57.0	15	53	US-10-708-953A-572403	Sequence 5	C 287	9.75	45.0	45.0	12	40	US-10-257-017B-338626	Sequence 3
C 215	11.4	76.0	57.0	15	53	US-10-708-953A-716806	Sequence 7	C 288	9.75	45.0	45.0	12	40	US-10-257-017B-342781	Sequence 3
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C 217	11.4	76.0	57.0	15	53	US-10-708-953A-1276947	Sequence 1	C 290	9.75	45.0	45.0	12	40	US-10-257-017B-345821	Sequence 3
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C 220	9.8	75.4	49.0	13	51	US-10-708-952A-102785	Sequence 1	C 293	9.75	45.0	45.0	12	40	US-10-257-017B-369254	Sequence 3
C 221	9.8	75.4	49.0	13	51	US-10-708-952A-105521	Sequence 1	C 294	9.75	45.0	45.0	12	40	US-10-257-017B-369635	Sequence 3
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C 226	9.8	75.4	49.0	13	51	US-10-708-952B-281446	Sequence 2	C 299	9.75	45.0	45.0	12	52	US-10-708-953-2107113	Sequence 2
C 227	9.8	75.4	49.0	13	51	US-10-708-952B-283324	Sequence 5	C 300	9.75	45.0	45.0	12	53	US-10-708-953A-1574359	Sequence 1
C 228	9.8	75.4	49.0	13	52	US-10-708-953-519962	Sequence 6	C 301	9.75	45.0	45.0	12	53	US-10-708-953A-1983714	Sequence 2
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310	10.4	74.3	52.0	14	53	US-10-708-953A-1763210	Sequence 1	383	8.8	73.3	44.0	12	47	US-10-477-086-15	Sequence 2
311	10.4	74.3	52.0	14	53	US-10-709-572-147851	Sequence 1	c 384	8.8	73.3	44.0	12	48	US-10-591-442-27	Sequence 2
312	10.4	74.3	52.0	14	57	US-10-799-238-14	Sequence 1	385	8.8	73.3	44.0	12	48	US-10-591-442-29	Sequence 4
313	9.6	73.8	48.0	13	40	US-10-257-017B-61663	Sequence 6	386	8.8	73.3	44.0	12	51	US-10-591-442-45	Sequence 1
314	9.6	73.8	48.0	13	40	US-10-257-017B-61664	Sequence 6	387	8.8	73.3	44.0	12	51	US-10-708-952A-111659	Sequence 4
315	11.8	73.8	59.0	16	1	PCT-US02-25943-533	Sequence 5	388	8.8	73.3	44.0	12	51	US-10-708-952A-289071	Sequence 2
316	11.8	73.8	59.0	16	30	US-09-708-690-5807	Sequence 5	389	8.8	73.3	44.0	12	51	US-10-708-952B-111659	Sequence 2
317	11.8	73.8	59.0	16	33	US-09-870-161-5807	Sequence 5	390	8.8	73.3	44.0	12	51	US-10-708-952B-289071	Sequence 2
318	11.8	73.8	59.0	16	40	US-10-227-565-533	Sequence 5	391	8.8	73.3	44.0	12	52	US-10-708-953-391440	Sequence 3
319	11.8	73.8	59.0	16	41	US-10-287-949A-5807	Sequence 5	392	8.8	73.3	44.0	12	52	US-10-708-953-426502	Sequence 4
320	11.8	73.8	59.0	16	41	US-10-287-949B-5807	Sequence 5	393	8.8	73.3	44.0	12	52	US-10-708-953-448734	Sequence 4
321	11.8	73.8	59.0	16	41	US-10-287-949C-5807	Sequence 5	394	8.8	73.3	44.0	12	52	US-10-708-953-451057	Sequence 4
322	11.8	73.8	59.0	16	46	US-10-367-832A-533	Sequence 5	395	8.8	73.3	44.0	12	52	US-10-708-953-467798	Sequence 4
323	11.8	73.8	59.0	16	53	US-10-709-572-191130	Sequence 1	396	8.8	73.3	44.0	12	52	US-10-708-953-524180	Sequence 5
324	11.8	73.8	59.0	16	53	US-10-709-572-191264	Sequence 1	397	8.8	73.3	44.0	12	52	US-10-708-953-580776	Sequence 5
325	11.8	73.8	59.0	16	63	US-11-088-219-5807	Sequence 1	398	8.8	73.3	44.0	12	52	US-10-708-953-752554	Sequence 7
326	11.8	73.8	59.0	16	63	US-11-088-219A-5807	Sequence 1	399	8.8	73.3	44.0	12	52	US-10-708-953-770756	Sequence 7
327	14	73.7	70.0	19	2	PCT-US03-36787-764639	Sequence 7	400	8.8	73.3	44.0	12	52	US-10-708-953-787100	Sequence 7
328	14	73.7	70.0	19	54	US-10-714-333A-764639	Sequence 7	401	8.8	73.3	44.0	12	52	US-10-708-953-863477	Sequence 8
329	14	73.7	70.0	19	55	US-10-714-333B-764639	Sequence 7	402	8.8	73.3	44.0	12	52	US-10-708-953-924430	Sequence 9
330	14	73.7	70.0	19	56	US-10-714-333C-764639	Sequence 7	403	8.8	73.3	44.0	12	52	US-10-708-953-925708	Sequence 9
331	14	73.7	70.0	19	63	US-11-083-784-764639	Sequence 7	404	8.8	73.3	44.0	12	52	US-10-708-953-958234	Sequence 1
332	14	73.7	70.0	19	64	US-11-093-832-764639	Sequence 7	405	8.8	73.3	44.0	12	52	US-10-708-953-1033680	Sequence 1
333	14	73.7	70.0	19	65	US-11-095-383-764639	Sequence 7	406	8.8	73.3	44.0	12	52	US-10-708-953-1041658	Sequence 1
334	14	73.7	70.0	19	66	US-11-101-244-764639	Sequence 7	407	8.8	73.3	44.0	12	52	US-10-708-953-1316830	Sequence 1
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342	11	73.3	55.0	15	21	US-09-274-553E-1284	Sequence 1	415	8.8	73.3	44.0	12	52	US-10-708-953-1868045	Sequence 1
343	11	73.3	55.0	15	24	US-09-504-231A-1284	Sequence 1	416	8.8	73.3	44.0	12	52	US-10-708-953-1868720	Sequence 2
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345	11	73.3	55.0	15	27	US-09-611-931-1284	Sequence 1	418	8.8	73.3	44.0	12	52	US-10-708-953-2054387	Sequence 2
346	11	73.3	55.0	15	27	US-09-611-931A-1284	Sequence 1	419	8.8	73.3	44.0	12	52	US-10-708-953-2142733	Sequence 2
347	11	73.3	55.0	15	30	US-09-708-690-4150	Sequence 4	420	8.8	73.3	44.0	12	52	US-10-708-953-2179457	Sequence 2
348	11	73.3	55.0	15	33	US-09-870-161-4150	Sequence 4	421	8.8	73.3	44.0	12	52	US-10-708-953-2206794	Sequence 3
349	11	73.3	55.0	15	41	US-10-287-949A-4150	Sequence 4	422	8.8	73.3	44.0	12	53	US-10-708-953A-391440	Sequence 4
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353	11	73.3	55.0	15	60	US-10-951-303B-4150	Sequence 4	426	8.8	73.3	44.0	12	53	US-10-708-953A-467798	Sequence 4
354	11	73.3	55.0	15	63	US-11-088-219-4150	Sequence 4	427	8.8	73.3	44.0	12	53	US-10-708-953A-524180	Sequence 5
355	11	73.3	55.0	15	63	US-11-088-219A-4150	Sequence 4	428	8.8	73.3	44.0	12	53	US-10-708-953A-580776	Sequence 5
356	8.8	73.3	44.0	12	1	PCT-IL05-00263-27	Sequence 2	429	8.8	73.3	44.0	12	53	US-10-708-953A-752554	Sequence 7
357	8.8	73.3	44.0	12	1	PCT-IL05-00263-29	Sequence 2	430	8.8	73.3	44.0	12	53	US-10-708-953A-770756	Sequence 7
358	8.8	73.3	44.0	12	1	PCT-IL05-00263-45	Sequence 4	431	8.8	73.3	44.0	12	53	US-10-708-953A-863477	Sequence 8
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362	8.8	73.3	44.0	12	3	PCT-US07-68403-1512	Sequence 1	435	8.8	73.3	44.0	12	53	US-10-708-953A-1033680	Sequence 1
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365	8.8	73.3	44.0	12	3	PCT-US07-68408-1512	Sequence 1	438	8.8	73.3	44.0	12	53	US-10-708-953A-1342582	Sequence 1
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367	8.8	73.3	44.0	12	3	PCT-US07-68412-1512	Sequence 1	440	8.8	73.3	44.0	12	53	US-10-708-953A-1380444	Sequence 1
368	8.8	73.3	44.0	12	21	US-09-229-591-33	Sequence 3	441	8.8	73.3	44.0	12	53	US-10-708-953A-1380444	Sequence 1
369	8.8	73.3	44.0	12	24	US-09-229-552-22	Sequence 2	442	8.8	73.3	44.0	12	53	US-10-708-953A-1393333	Sequence 1
370	8.8	73.3	44.0	12	38	US-10-004-382-22	Sequence 2	443	8.8	73.3	44.0	12	53	US-10-708-953A-1669231	Sequence 1
371	8.8	73.3	44.0	12	40	US-10-257-017B-275104	Sequence 2	444	8.8	73.3	44.0	12	53	US-10-708-953A-1699231	Sequence 1
372	8.8	73.3	44.0	12	40	US-10-257-017B-290891	Sequence 2	445	8.8	73.3	44.0	12	53	US-10-708-953A-1754748	Sequence 1
373	8.8	73.3	44.0	12	40	US-10-257-017B-317181	Sequence 3	446	8.8	73.3	44.0	12	53	US-10-708-953A-1858055	Sequence 1
374	8.8	73.3	44.0	12	40	US-10-257-017B-322885	Sequence 3	447	8.8	73.3	44.0	12	53	US-10-708-953A-1868045	Sequence 1
375	8.8	73.3	44.0	12	40	US-10-257-017B-323132	Sequence 3	448	8.8	73.3	44.0	12	53	US-10-708-953A-1868720	Sequence 2
376	8.8	73.3	44.0	12	40	US-10-257-017B-326883	Sequence 3	449	8.8	73.3	44.0	12	53	US-10-708-953A-2003791	Sequence 2
377	8.8	73.3	44.0	12	40	US-10-257-017B-327149	Sequence 3	450	8.8	73.3	44.0	12	53	US-10-708-953A-2054387	Sequence 2
378	8.8	73.3	44.0	12	40	US-10-257-017B-327149	Sequence 3	450	8.8	73.3	44.0	12	53	US-10-708-953A-2142733	Sequence 2



C 451	8.8	73.3	44.0	12	53	US-10-708-953A-2179457	Sequence 2	524	9.4	72.3	47.0	13	51	US-10-708-952B-364482	Sequence 3
C 452	8.8	73.3	44.0	12	53	US-10-708-953A-2206794	Sequence 2	525	9.4	72.3	47.0	13	52	US-10-708-953-407469	Sequence 4
C 453	8.8	73.3	44.0	12	53	US-10-708-952-190034	Sequence 1	C 526	9.4	72.3	47.0	13	52	US-10-708-953-470264	Sequence 4
C 454	8.8	73.3	44.0	12	53	US-10-708-952-225526	Sequence 2	C 527	9.4	72.3	47.0	13	52	US-10-708-953-470264	Sequence 4
C 455	8.8	73.3	44.0	12	53	US-10-708-952-258617	Sequence 2	528	9.4	72.3	47.0	13	52	US-10-708-953-472685	Sequence 5
C 456	8.8	73.3	44.0	12	53	US-10-708-952-260004	Sequence 1	529	9.4	72.3	47.0	13	52	US-10-708-953-524505	Sequence 5
C 457	8.8	73.3	44.0	12	66	US-11-126-421-15	Sequence 1	530	9.4	72.3	47.0	13	52	US-10-708-953-578960	Sequence 5
C 458	8.8	73.3	44.0	12	75	US-11-438-135-357	Sequence 3	531	9.4	72.3	47.0	13	52	US-10-708-953-753472	Sequence 7
C 459	8.8	73.3	44.0	12	75	US-11-438-135-358	Sequence 3	532	9.4	72.3	47.0	13	52	US-10-708-953-804253	Sequence 8
C 460	8.8	73.3	44.0	12	78	US-11-588-939A-7	Sequence 7	533	9.4	72.3	47.0	13	52	US-10-708-953-869690	Sequence 8
C 461	8.8	73.3	44.0	12	81	US-11-745-429-1512	Sequence 1	534	9.4	72.3	47.0	13	52	US-10-708-953-956183	Sequence 9
C 462	8.8	73.3	44.0	12	81	US-11-799-117-48	Sequence 4	535	9.4	72.3	47.0	13	52	US-10-708-953-1053507	Sequence 1
C 463	8.8	73.3	44.0	12	87	US-60-244-692-22	Sequence 2	536	9.4	72.3	47.0	13	52	US-10-708-953-1090140	Sequence 1
C 464	12.4	72.9	62.0	17	25	US-09-546-745A-4860	Sequence 4	C 537	9.4	72.3	47.0	13	52	US-10-708-953-1150335	Sequence 1
C 465	12.4	72.9	62.0	17	25	US-09-546-745A-4861	Sequence 4	C 538	9.4	72.3	47.0	13	52	US-10-708-953-1181122	Sequence 1
C 466	12.4	72.9	62.0	17	49	US-10-608-923-508977	Sequence 5	C 539	9.4	72.3	47.0	13	52	US-10-708-953-1188461	Sequence 1
C 467	16	72.7	80.0	22	3	PCT-US05-37925-39	Sequence 3	C 540	9.4	72.3	47.0	13	52	US-10-708-953-1199339	Sequence 1
C 468	16	72.7	80.0	22	3	PCT-US05-37925-51	Sequence 5	541	9.4	72.3	47.0	13	52	US-10-708-953-1341689	Sequence 1
C 469	16	72.7	80.0	22	3	PCT-US06-00086-6	Sequence 6	542	9.4	72.3	47.0	13	52	US-10-708-953-1437920	Sequence 1
C 470	13.8	72.6	69.0	19	49	US-10-605-923-810848	Sequence 8	C 543	9.4	72.3	47.0	13	52	US-10-708-953-1484405	Sequence 1
C 471	13.8	72.6	69.0	19	50	US-10-605-924-801404	Sequence 8	544	9.4	72.3	47.0	13	52	US-10-708-953-1508698	Sequence 1
C 472	9.4	72.3	47.0	13	24	US-09-528-209A-6207	Sequence 6	C 545	9.4	72.3	47.0	13	52	US-10-708-953-1540033	Sequence 1
C 473	9.4	72.3	47.0	13	40	US-10-257-017B-6223	Sequence 6	546	9.4	72.3	47.0	13	52	US-10-708-953-1642533	Sequence 1
C 474	9.4	72.3	47.0	13	40	US-10-257-017B-6224	Sequence 6	547	9.4	72.3	47.0	13	52	US-10-708-953-1648335	Sequence 1
C 475	9.4	72.3	47.0	13	40	US-10-257-017B-12629	Sequence 1	C 548	9.4	72.3	47.0	13	52	US-10-708-953-1676486	Sequence 1
C 476	9.4	72.3	47.0	13	40	US-10-257-017B-12630	Sequence 1	549	9.4	72.3	47.0	13	52	US-10-708-953-1731944	Sequence 1
C 477	9.4	72.3	47.0	13	40	US-10-257-017B-12630	Sequence 1	550	9.4	72.3	47.0	13	52	US-10-708-953-174724	Sequence 1
C 478	9.4	72.3	47.0	13	40	US-10-257-017B-25055	Sequence 2	551	9.4	72.3	47.0	13	52	US-10-708-953-1747813	Sequence 1
C 479	9.4	72.3	47.0	13	40	US-10-257-017B-25056	Sequence 2	552	9.4	72.3	47.0	13	52	US-10-708-953-1765468	Sequence 1
C 480	9.4	72.3	47.0	13	40	US-10-257-017B-25081	Sequence 2	C 553	9.4	72.3	47.0	13	52	US-10-708-953-1847452	Sequence 1
C 481	9.4	72.3	47.0	13	40	US-10-257-017B-25082	Sequence 2	554	9.4	72.3	47.0	13	52	US-10-708-953-1859282	Sequence 1
C 482	9.4	72.3	47.0	13	40	US-10-257-017B-27969	Sequence 2	C 554	9.4	72.3	47.0	13	52	US-10-708-953-1859282	Sequence 1
C 483	9.4	72.3	47.0	13	40	US-10-257-017B-27970	Sequence 2	555	9.4	72.3	47.0	13	52	US-10-708-953-1969357	Sequence 1
C 484	9.4	72.3	47.0	13	40	US-10-257-017B-36537	Sequence 3	C 556	9.4	72.3	47.0	13	52	US-10-708-953-1981793	Sequence 1
C 485	9.4	72.3	47.0	13	40	US-10-257-017B-36538	Sequence 3	557	9.4	72.3	47.0	13	52	US-10-708-953-1988331	Sequence 1
C 486	9.4	72.3	47.0	13	40	US-10-257-017B-56753	Sequence 5	C 558	9.4	72.3	47.0	13	52	US-10-708-953-2045464	Sequence 2
C 487	9.4	72.3	47.0	13	40	US-10-257-017B-56754	Sequence 5	559	9.4	72.3	47.0	13	52	US-10-708-953-2074065	Sequence 2
C 488	9.4	72.3	47.0	13	40	US-10-257-017B-96865	Sequence 9	C 560	9.4	72.3	47.0	13	52	US-10-708-953-2105665	Sequence 2
C 489	9.4	72.3	47.0	13	40	US-10-257-017B-96866	Sequence 9	561	9.4	72.3	47.0	13	52	US-10-708-953-2145797	Sequence 2
C 490	9.4	72.3	47.0	13	40	US-10-257-017B-111321	Sequence 1	C 562	9.4	72.3	47.0	13	52	US-10-708-953-2156391	Sequence 2
C 491	9.4	72.3	47.0	13	40	US-10-257-017B-111322	Sequence 1	563	9.4	72.3	47.0	13	52	US-10-708-953-2195838	Sequence 2
C 492	9.4	72.3	47.0	13	40	US-10-257-017B-117287	Sequence 1	C 564	9.4	72.3	47.0	13	52	US-10-708-953-2219670	Sequence 2
C 493	9.4	72.3	47.0	13	40	US-10-257-017B-117288	Sequence 1	565	9.4	72.3	47.0	13	53	US-10-708-953A-407469	Sequence 4
C 494	9.4	72.3	47.0	13	40	US-10-257-017B-117509	Sequence 1	C 566	9.4	72.3	47.0	13	53	US-10-708-953A-447891	Sequence 4
C 495	9.4	72.3	47.0	13	40	US-10-257-017B-117510	Sequence 1	567	9.4	72.3	47.0	13	53	US-10-708-953A-470264	Sequence 4
C 496	9.4	72.3	47.0	13	40	US-10-257-017B-187027	Sequence 1	C 568	9.4	72.3	47.0	13	53	US-10-708-953A-472685	Sequence 4
C 497	9.4	72.3	47.0	13	40	US-10-257-017B-187028	Sequence 1	569	9.4	72.3	47.0	13	53	US-10-708-953A-524505	Sequence 5
C 498	9.4	72.3	47.0	13	40	US-10-257-017B-215785	Sequence 2	C 570	9.4	72.3	47.0	13	53	US-10-708-953A-578960	Sequence 5
C 499	9.4	72.3	47.0	13	40	US-10-257-017B-215786	Sequence 2	571	9.4	72.3	47.0	13	53	US-10-708-953A-753472	Sequence 7
C 500	9.4	72.3	47.0	13	40	US-10-257-017B-235787	Sequence 2	C 572	9.4	72.3	47.0	13	53	US-10-708-953A-804253	Sequence 8
C 501	9.4	72.3	47.0	13	40	US-10-257-017B-235788	Sequence 2	573	9.4	72.3	47.0	13	53	US-10-708-953A-869690	Sequence 8
C 502	9.4	72.3	47.0	13	40	US-10-257-017B-248349	Sequence 2	C 574	9.4	72.3	47.0	13	53	US-10-708-953A-956183	Sequence 9
C 503	9.4	72.3	47.0	13	40	US-10-257-017B-248350	Sequence 2	575	9.4	72.3	47.0	13	53	US-10-708-953A-1053507	Sequence 1
C 504	9.4	72.3	47.0	13	51	US-10-708-952A-214716	Sequence 2	C 576	9.4	72.3	47.0	13	53	US-10-708-953A-1090140	Sequence 1
C 505	9.4	72.3	47.0	13	51	US-10-708-952A-215927	Sequence 2	C 577	9.4	72.3	47.0	13	53	US-10-708-953A-1150335	Sequence 1
C 506	9.4	72.3	47.0	13	51	US-10-708-952A-217181	Sequence 2	C 578	9.4	72.3	47.0	13	53	US-10-708-953A-1181122	Sequence 1
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C 509	9.4	72.3	47.0	13	51	US-10-708-952A-221139	Sequence 2	C 581	9.4	72.3	47.0	13	53	US-10-708-953A-1341689	Sequence 1
C 510	9.4	72.3	47.0	13	51	US-10-708-952A-226704	Sequence 2	582	9.4	72.3	47.0	13	53	US-10-708-953A-1437920	Sequence 1
C 511	9.4	72.3	47.0	13	51	US-10-708-952A-252681	Sequence 2	C 583	9.4	72.3	47.0	13	53	US-10-708-953A-1484405	Sequence 1
C 512	9.4	72.3	47.0	13	51	US-10-708-952A-260591	Sequence 2	584	9.4	72.3	47.0	13	53	US-10-708-953A-1508698	Sequence 1
C 513	9.4	72.3	47.0	13	51	US-10-708-952A-272157	Sequence 2	C 585	9.4	72.3	47.0	13	53	US-10-708-953A-1540033	Sequence 1
C 514	9.4	72.3	47.0	13	51	US-10-708-952A-364482	Sequence 3	586	9.4	72.3	47.0	13	53	US-10-708-953A-1642533	Sequence 1
C 515	9.4	72.3	47.0	13	51	US-10-708-952B-214716	Sequence 2	C 587	9.4	72.3	47.0	13	53	US-10-708-953A-1648335	Sequence 1
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C 602	9.4	72.3	47.0	13	53	US-10-708-953A-2156391	Sequence 2	C 675	10	71.4	50.0	14	53	US-10-708-953A-1161164	Sequence 1
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C 609	9.4	72.3	47.0	13	53	US-10-708-953A-325219	Sequence 3	C 682	12.8	71.1	64.0	18	50	US-10-605-924-1258144	Sequence 1
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C 612	10.8	72.0	54.0	15	1	PCT-US02-25944-4166	Sequence 4	C 685	12.8	71.1	64.0	18	63	US-11-084-847-541	Sequence 9
C 613	10.8	72.0	54.0	15	1	PCT-US02-25944-4198	Sequence 1	C 686	17	70.8	85.0	24	3	PCT-US06-00086-9	Sequence 1
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C 616	10.8	72.0	54.0	15	40	US-10-227-564-4166	Sequence 4	C 689	10.6	70.7	53.0	15	39	US-10-160-358-26	Sequence 3
C 617	10.8	72.0	54.0	15	40	US-10-227-564-4198	Sequence 4	C 690	12	70.6	60.0	17	1	PCT-US02-17674-3654	Sequence 1
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C 619	10.8	72.0	54.0	15	46	US-10-321-854-2304	Sequence 2	C 692	12	70.6	60.0	17	30	US-09-708-690-1647	Sequence 6
C 620	10.8	72.0	54.0	15	46	US-10-364-412A-4166	Sequence 4	C 693	12	70.6	60.0	17	30	US-09-708-690-6253	Sequence 6
C 621	10.8	72.0	54.0	15	46	US-10-364-412A-4198	Sequence 4	C 694	12	70.6	60.0	17	30	US-09-708-690-6254	Sequence 8
C 622	10.8	72.0	54.0	15	46	US-10-367-892-144	Sequence 1	C 695	12	70.6	60.0	17	33	US-09-870-161-1646	Sequence 1
C 623	10.8	72.0	54.0	15	46	US-10-367-892-2982	Sequence 2	C 696	12	70.6	60.0	17	33	US-09-870-161-1647	Sequence 1
C 624	10.8	72.0	54.0	15	49	US-10-604-985-8387	Sequence 8	C 697	12	70.6	60.0	17	33	US-09-870-161-1647	Sequence 6
C 625	10.8	72.0	54.0	15	49	US-10-604-985A-8387	Sequence 8	C 698	12	70.6	60.0	17	33	US-09-870-161-6253	Sequence 6
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C 628	10.8	72.0	54.0	15	51	US-10-708-952A-105423	Sequence 2	C 701	12	70.6	60.0	17	41	US-10-287-949A-1646	Sequence 1
C 629	10.8	72.0	54.0	15	51	US-10-708-952A-282645	Sequence 2	C 702	12	70.6	60.0	17	41	US-10-287-949A-1647	Sequence 1
C 630	10.8	72.0	54.0	15	51	US-10-708-952A-284070	Sequence 2	C 703	12	70.6	60.0	17	41	US-10-287-949A-6253	Sequence 6
C 631	10.8	72.0	54.0	15	51	US-10-708-952B-104569	Sequence 1	C 704	12	70.6	60.0	17	41	US-10-287-949A-6254	Sequence 6
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C 634	10.8	72.0	54.0	15	52	US-10-708-953-545642	Sequence 5	C 707	12	70.6	60.0	17	41	US-10-287-949B-6253	Sequence 6
C 635	10.8	72.0	54.0	15	52	US-10-708-953-1724380	Sequence 1	C 708	12	70.6	60.0	17	41	US-10-287-949B-6254	Sequence 6
C 636	10.8	72.0	54.0	15	52	US-10-708-953-2042003	Sequence 2	C 709	12	70.6	60.0	17	41	US-10-287-949B-6254	Sequence 8
C 637	10.8	72.0	54.0	15	52	US-10-708-953-2053033	Sequence 3	C 710	12	70.6	60.0	17	41	US-10-287-949C-1646	Sequence 1
C 638	10.8	72.0	54.0	15	53	US-10-708-953A-1724380	Sequence 1	C 711	12	70.6	60.0	17	41	US-10-287-949C-1647	Sequence 1
C 639	10.8	72.0	54.0	15	53	US-10-708-953A-2042003	Sequence 2	C 712	12	70.6	60.0	17	41	US-10-287-949C-6253	Sequence 6
C 640	10.8	72.0	54.0	15	53	US-10-708-953A-2042003	Sequence 2	C 713	12	70.6	60.0	17	41	US-10-287-949C-6254	Sequence 6
C 641	10.8	72.0	54.0	15	53	US-10-708-953A-2053033	Sequence 1	C 714	12	70.6	60.0	17	41	US-10-287-949C-6254	Sequence 8
C 642	10.8	72.0	54.0	15	53	US-10-708-953A-2053033	Sequence 1	C 715	12	70.6	60.0	17	41	US-10-287-949C-8571	Sequence 3
C 643	10.8	72.0	54.0	15	53	US-10-709-572-159335	Sequence 2	C 716	12	70.6	60.0	17	53	US-10-712-633-3654	Sequence 1
C 644	10.8	72.0	54.0	15	53	US-10-709-572-203706	Sequence 2	C 717	12	70.6	60.0	17	60	US-10-951-303-1647	Sequence 1
C 645	10.8	72.0	54.0	15	58	US-10-834-967-1289	Sequence 4	C 718	12	70.6	60.0	17	60	US-10-951-303B-1646	Sequence 1
C 646	10.8	72.0	54.0	15	58	US-10-834-967-4959	Sequence 4	C 719	12	70.6	60.0	17	60	US-10-951-303B-1647	Sequence 1
C 647	12.2	71.8	61.0	17	41	US-10-299-054A-2636	Sequence 2	C 720	12	70.6	60.0	17	63	US-11-088-219-1647	Sequence 1
C 648	12.2	71.8	61.0	17	49	US-10-605-923-1392765	Sequence 1	C 721	12	70.6	60.0	17	63	US-11-088-219-1647	Sequence 1
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C 650	10	71.4	50.0	14	3	PCT-US07-68402-329	Sequence 3	C 723	12	70.6	60.0	17	63	US-11-088-219-6253	Sequence 6
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C 652	10	71.4	50.0	14	3	PCT-US07-68404-329	Sequence 3	C 725	12	70.6	60.0	17	63	US-11-088-219-8571	Sequence 1
C 653	10	71.4	50.0	14	3	PCT-US07-68406-329	Sequence 3	C 726	12	70.6	60.0	17	63	US-11-088-219A-1646	Sequence 1
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C 655	10	71.4	50.0	14	3	PCT-US07-68410-329	Sequence 3	C 728	12	70.6	60.0	17	63	US-11-088-219A-6253	Sequence 6
C 656	10	71.4	50.0	14	3	PCT-US07-68412-329	Sequence 3	C 729	12	70.6	60.0	17	63	US-11-088-219A-6254	Sequence 8
C 657	10	71.4	50.0	14	14	US-08-591-486B-34	Sequence 3	C 730	12	70.6	60.0	17	63	US-11-088-219A-8571	Sequence 8
C 658	10	71.4	50.0	14	14	US-08-591-486B-34	Sequence 3	C 731	12	70.6	60.0	17	76	US-11-475-062-8179	Sequence 7
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C 660	10	71.4	50.0	14	51	US-10-708-952A-180197	Sequence 1	C 733	13.4	70.5	67.0	19	2	PCT-US03-36787-726385	Sequence 1
C 661	10	71.4	50.0	14	51	US-10-708-952A-348556	Sequence 3	C 734	13.4	70.5	67.0	19	2	PCT-US03-36787-1192689	Sequence 1
C 662	10	71.4	50.0	14	51	US-10-708-952A-349080	Sequence 3	C 735	13.4	70.5	67.0	19	2	PCT-US03-36787-1192696	Sequence 1
C 663	10	71.4	50.0	14	51	US-10-708-952B-178861	Sequence 1	C 736	13.4	70.5	67.0	19	2	PCT-US03-36787-1192704	Sequence 1
C 664	10	71.4	50.0	14	51	US-10-708-952B-180197	Sequence 1	C 737	13.4	70.5	67.0	19	50	US-10-605-924-1191074	Sequence 1
C 665	10	71.4	50.0	14	51	US-10-708-952B-348556	Sequence 3	C 738	13.4	70.5	67.0	19	54	US-10-714-333A-726378	Sequence 7
C 666	10	71.4	50.0	14	51	US-10-708-952B-349080	Sequence 3	C 739	13.4	70.5	67.0	19	54	US-10-714-333A-726385	Sequence 1
C 667	10	71.4	50.0	14	52	US-10-708-953-559363	Sequence 5	C 740	13.4	70.5	67.0	19	54	US-10-714-333A-1192689	Sequence 1
C 668	10	71.4	50.0	14	52	US-10-708-953-809991	Sequence 8	C 741	13.4	70.5	67.0	19	54	US-10-714-333A-1192696	Sequence 1
C 669	10	71.4	50.0	14	52	US-10-708-953-1161164	Sequence 1	C 742	13.4	70.5	67.0	19	54	US-10-714-333A-1192704	Sequence 1

C 743	13.4	70.5	67.0	19	55	US-10-714-333B-726378	Sequence 7	C 816	9.8	70.0	49.0	14	52	US-10-708-953-756503	Sequence 7
C 744	13.4	70.5	67.0	19	55	US-10-714-333B-726385	Sequence 7	C 817	9.8	70.0	49.0	14	52	US-10-708-953-787966	Sequence 7
C 745	13.4	70.5	67.0	19	55	US-10-714-333B-1192689	Sequence 1	818	9.8	70.0	49.0	14	52	US-10-708-953-801220	Sequence 8
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C 747	13.4	70.5	67.0	19	55	US-10-714-333B-1192704	Sequence 1	820	9.8	70.0	49.0	14	52	US-10-708-953-930627	Sequence 8
C 748	13.4	70.5	67.0	19	56	US-10-714-333C-726378	Sequence 7	C 821	9.8	70.0	49.0	14	52	US-10-708-953-1000343	Sequence 1
C 749	13.4	70.5	67.0	19	56	US-10-714-333C-726385	Sequence 7	C 822	9.8	70.0	49.0	14	52	US-10-708-953-1132564	Sequence 1
C 750	13.4	70.5	67.0	19	56	US-10-714-333C-1192689	Sequence 1	C 823	9.8	70.0	49.0	14	52	US-10-708-953-1188181	Sequence 1
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C 752	13.4	70.5	67.0	19	56	US-10-714-333C-1192704	Sequence 1	C 825	9.8	70.0	49.0	14	52	US-10-708-953-1317930	Sequence 1
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C 761	13.4	70.5	67.0	19	64	US-11-093-832-1192696	Sequence 1	C 834	9.8	70.0	49.0	14	52	US-10-708-953-1840939	Sequence 1
C 762	13.4	70.5	67.0	19	64	US-11-093-832-1192704	Sequence 1	C 835	9.8	70.0	49.0	14	52	US-10-708-953-1857310	Sequence 1
C 763	13.4	70.5	67.0	19	65	US-11-095-383-726378	Sequence 7	C 836	9.8	70.0	49.0	14	52	US-10-708-953-1875033	Sequence 1
C 764	13.4	70.5	67.0	19	65	US-11-095-383-726385	Sequence 7	C 837	9.8	70.0	49.0	14	52	US-10-708-953-1875410	Sequence 1
C 765	13.4	70.5	67.0	19	65	US-11-095-383-1192689	Sequence 1	C 838	9.8	70.0	49.0	14	52	US-10-708-953-1971834	Sequence 1
C 766	13.4	70.5	67.0	19	65	US-11-095-383-1192696	Sequence 1	C 839	9.8	70.0	49.0	14	52	US-10-708-953-2125666	Sequence 2
C 767	13.4	70.5	67.0	19	65	US-11-095-383-1192704	Sequence 1	C 840	9.8	70.0	49.0	14	52	US-10-708-953-2228733	Sequence 2
C 768	13.4	70.5	67.0	19	66	US-11-101-244-726378	Sequence 7	C 841	9.8	70.0	49.0	14	53	US-10-708-953A-418459	Sequence 4
C 769	13.4	70.5	67.0	19	66	US-11-101-244-726385	Sequence 7	C 842	9.8	70.0	49.0	14	53	US-10-708-953A-438494	Sequence 4
C 770	13.4	70.5	67.0	19	66	US-11-101-244-1192689	Sequence 1	C 843	9.8	70.0	49.0	14	53	US-10-708-953A-549103	Sequence 5
C 771	13.4	70.5	67.0	19	66	US-11-101-244-1192696	Sequence 1	C 844	9.8	70.0	49.0	14	53	US-10-708-953A-591354	Sequence 5
C 772	13.4	70.5	67.0	19	66	US-11-101-244-1192704	Sequence 1	C 845	9.8	70.0	49.0	14	53	US-10-708-953A-610006	Sequence 6
C 773	13.4	70.5	67.0	19	71	US-11-313-452-726378	Sequence 7	C 846	9.8	70.0	49.0	14	53	US-10-708-953A-651771	Sequence 6
C 774	13.4	70.5	67.0	19	71	US-11-313-452-726385	Sequence 7	C 847	9.8	70.0	49.0	14	53	US-10-708-953A-756503	Sequence 7
C 775	13.4	70.5	67.0	19	71	US-11-313-452-1192689	Sequence 1	C 848	9.8	70.0	49.0	14	53	US-10-708-953A-787966	Sequence 7
C 776	13.4	70.5	67.0	19	71	US-11-313-452-1192696	Sequence 1	C 849	9.8	70.0	49.0	14	53	US-10-708-953A-801220	Sequence 8
C 777	13.4	70.5	67.0	19	71	US-11-313-452-1192704	Sequence 1	C 850	9.8	70.0	49.0	14	53	US-10-708-953A-858747	Sequence 8
C 778	13.4	70.5	67.0	19	72	US-11-313-452A-726378	Sequence 7	C 851	9.8	70.0	49.0	14	53	US-10-708-953A-930627	Sequence 9
C 779	13.4	70.5	67.0	19	72	US-11-313-452A-726385	Sequence 7	C 852	9.8	70.0	49.0	14	53	US-10-708-953A-1000343	Sequence 1
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C 782	13.4	70.5	67.0	19	72	US-11-313-452A-1192704	Sequence 1	C 855	9.8	70.0	49.0	14	53	US-10-708-953A-1250851	Sequence 1
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C 786	11.2	70.0	56.0	16	46	US-10-367-832A-20371	Sequence 2	C 859	9.8	70.0	49.0	14	53	US-10-708-953A-1409428	Sequence 1
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C 790	9.8	70.0	49.0	14	51	US-10-708-952A-103254	Sequence 1	C 863	9.8	70.0	49.0	14	53	US-10-708-953A-1777980	Sequence 1
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C 793	9.8	70.0	49.0	14	51	US-10-708-952A-130975	Sequence 1	C 866	9.8	70.0	49.0	14	53	US-10-708-953A-1840939	Sequence 1
C 794	9.8	70.0	49.0	14	51	US-10-708-952A-132354	Sequence 1	C 867	9.8	70.0	49.0	14	53	US-10-708-953A-1857310	Sequence 1
C 795	9.8	70.0	49.0	14	51	US-10-708-952A-282060	Sequence 2	C 868	9.8	70.0	49.0	14	53	US-10-708-953A-1875410	Sequence 1
C 796	9.8	70.0	49.0	14	51	US-10-708-952A-284069	Sequence 2	C 869	9.8	70.0	49.0	14	53	US-10-708-953A-2125666	Sequence 2
C 797	9.8	70.0	49.0	14	51	US-10-708-952A-288500	Sequence 2	C 870	9.8	70.0	49.0	14	53	US-10-708-953A-2198709	Sequence 2
C 798	9.8	70.0	49.0	14	51	US-10-708-952A-303863	Sequence 3	C 871	9.8	70.0	49.0	14	53	US-10-708-953A-2228733	Sequence 2
C 799	9.8	70.0	49.0	14	51	US-10-708-952A-304724	Sequence 3	C 872	9.8	70.0	49.0	14	53	US-10-709-572-142720	Sequence 1
C 800	9.8	70.0	49.0	14	51	US-10-708-952B-102561	Sequence 1	C 873	9.8	70.0	49.0	14	53	US-10-709-572-157982	Sequence 1
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C 807	9.8	70.0	49.0	14	51	US-10-708-952B-288500	Sequence 2	C 880	9.8	70.0	49.0	14	53	US-10-709-572-332589	Sequence 3
C 808	9.8	70.0	49.0	14	51	US-10-708-952B-303863	Sequence 3	881	9.8	70.0	49.0	12	3	PCT-US96-03186-16	Sequence 1
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C 811	9.8	70.0	49.0	14	52	US-10-708-953-438494	Sequence 4	C 884	8.4	70.0	42.0	12	16	US-08-784-200A-24	Sequence 2
C 812	9.8	70.0	49.0	14	52	US-10-708-953-549103	Sequence 5	C 885	8.4	70.0	42.0	12	17	US-08-883-128-16	Sequence 2
C 813	9.8	70.0	49.0	14	52	US-10-708-953-591354	Sequence 5	C 886	8.4	70.0	42.0	12	21	US-09-254-929-33	Sequence 3
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C 893	8.4	70.0	42.0	12	40	US-10-257-017B-272438	Sequence 2
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C 903	8.4	70.0	42.0	12	40	US-10-257-017B-288407	Sequence 2
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ALIGNMENTS

RESULT 1  
PCT-US02-22417-64  
; Sequence 64, Application PC/TUS0222417  
; GENERAL INFORMATION:  
; APPLICANT: Andrew T. Watt  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTSP-0395  
; CURRENT APPLICATION NUMBER: PCT/US02/22417  
; CURRENT FILING DATE: 2002-07-13  
; PRIOR APPLICATION NUMBER: 09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 64  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
PCT-US02-22417-64

Query Match 100.0%; Score 20; DB 1; Length 20;  
Score over Length 100.0%;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCCCAGTGGAGTGGCGT 20  
|||||

Db 1 GCCCCAGTTGAAGTTGCCGT 20

## RESULT 2

US-09-908-147-64  
; Sequence 64, Application US/09908147  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/09/908,147  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 64  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
PCT-US02-22417-64

Query Match 100.0%; Score 20; DB 34; Length 20;  
Score over Length 100.0%;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCCGT 20  
|||||  
Db 1 GCCCCAGTTGAAGTTGCCGT 20

## RESULT 3

US-10-728-509-64  
; Sequence 64, Application US/10728509  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 64  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-728-509-64

Query Match 100.0%; Score 20; DB 56; Length 20;  
Score over Length 100.0%;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCCGT 20  
|||||  
Db 1 GCCCCAGTTGAAGTTGCCGT 20

## RESULT 4

PCT-US02-22417-65  
; Sequence 65, Application PC/TUS0222417  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0395  
; CURRENT APPLICATION NUMBER: PCT/US02/22417

; CURRENT FILING DATE: 2002-07-13  
; PRIOR APPLICATION NUMBER: 09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 65  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
PCT-US02-22417-65

Query Match 90.0%; Score 18; DB 1; Length 20;  
Score over Length 90.0%;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCC 18  
|||||  
Db 3 GCCCCAGTTGAAGTTGCC 20

## RESULT 5

US-09-908-147-65  
; Sequence 65, Application US/09908147  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/09/908,147  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 65  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-908-147-65

Query Match 90.0%; Score 18; DB 34; Length 20;  
Score over Length 90.0%;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCC 18  
|||||  
Db 3 GCCCCAGTTGAAGTTGCC 20

## RESULT 6

US-10-728-509-65  
; Sequence 65, Application US/10728509  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 65  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-728-509-65

Query Match 90.0%; Score 18; DB 56; Length 20;

```
Score over Length      90.0%;      Pred. No. 3.5e+02;
Best Local Similarity  100.0%;      Mismatches 0; Gaps 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTTGCC 18
DB 3 GCCCCAGTTGAAGTTGCC 20

RESULT 7
US-10-708-953-393940
; Sequence 393940, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 393940
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-393940

Query Match      57.0%;      Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%;      Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
DB 1 GCCCCACUUGAAG 13

RESULT 8
US-10-708-953-423956
; Sequence 423956, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 423956
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-423956

Query Match      57.0%;      Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%;      Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
DB 1 GCCCCACUUGAAG 13

RESULT 9
US-10-708-953-580710
; Sequence 580710, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
```

```
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 580710
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-580710
```

```
Query Match      57.0%;      Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%;      Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
DB 1 GCCCCACUUGAAG 13
```

```
RESULT 10
US-10-708-953-801440
; Sequence 801440, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 801440
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-801440
```

```
Query Match      57.0%;      Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%;      Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GCCCCAGTTGAAG 13
DB 1 GCCCCACUUGAAG 13
```

```
RESULT 11
US-10-708-953-1058146
; Sequence 1058146, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1058146
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1058146
```

```
Query Match      57.0%;      Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%;      Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
DB 1 GCCCCACUUGAAG 13
```

```
Db      1  GCCCCACUUGAAG 13

RESULT 12
US-10-708-953-1198625
; Sequence 1198625, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1198625
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1198625

Query Match      57.0%; Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 13
US-10-708-953-2178793
; Sequence 2178793, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2178793
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2178793

Query Match      57.0%; Score 11.4; DB 52; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 14
US-10-708-953A-393940
; Sequence 393940, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 393940
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-393940

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 15
US-10-708-953A-423956
; Sequence 423956, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 423956
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-423956

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 16
US-10-708-953A-580710
; Sequence 580710, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 580710
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-580710

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAAG 13
      ||||| :|||
Db      1  GCCCCACUUGAAG 13

RESULT 17
US-10-708-953A-801440
; Sequence 801440, Application US/10708953A
```

```
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 801440
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-801440

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGCCAGTTGAAG 13
      ||||| :|||
Db      1 GCGCCACUUGAAG 13

RESULT 18
US-10-708-953A-1058146
; Sequence 1058146, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1058146
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1058146

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGCCAGTTGAAG 13
      ||||| :|||
Db      1 GCGCCACUUGAAG 13

RESULT 19
US-10-708-953A-1198625
; Sequence 1198625, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1198625
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1198625

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
```

```
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGCCAGTTGAAG 13
      ||||| :|||
Db      1 GCGCCACUUGAAG 13

RESULT 20
US-10-708-953A-2178793
; Sequence 2178793, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2178793
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2178793

Query Match      57.0%; Score 11.4; DB 53; Length 13;
Score over Length 87.7%;
Best Local Similarity 76.9%; Pred. No. 7.7e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGCCAGTTGAAG 13
      ||||| :|||
Db      1 GCGCCACUUGAAG 13

RESULT 21
PCT-US02-25942-1071/c
; Sequence 1071, Application PC/TUS0225942
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25942
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1071
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 157
PCT-US02-25942-1071

Query Match      65.0%; Score 13; DB 1; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCGCCAGTTGAAG 13
      ||||| :|||
Db      13 GCGCCAGTTGAAG 1

RESULT 22
PCT-US02-25942-1072
; Sequence 1072, Application PC/TUS0225942
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
```



```

; CURRENT APPLICATION NUMBER: PCT/US02/25942
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1072
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 156
PCT-US02-25942-1072

Query Match      65.0%; Score 13; DB 1; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCAGTTGAAG 15

RESULT 23
PCT-US02-25942-1973/c
; Sequence 1973, Application PC/TUS0225942
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25942
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1973
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (2790547)...(2790562)
; OTHER INFORMATION: Chromosome = 3 Strand = positive ConnectronObjectNumber = 17163
PCT-US02-25942-1973

Query Match      65.0%; Score 13; DB 1; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCAGTTGAAG 15

RESULT 24
US-10-227-567-1071/c
; Sequence 1071, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1071
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 157
US-10-227-567-1071

Query Match      65.0%; Score 13; DB 1; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCAGTTGAAG 15

RESULT 25
US-10-227-567-1072
; Sequence 1072, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1072
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 156
US-10-227-567-1072

Query Match      65.0%; Score 13; DB 40; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 13 GCCCCAGTTGAAG 1

RESULT 26
US-10-227-567-1973/c
; Sequence 1973, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1973
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (2790547)...(2790562)
; OTHER INFORMATION: Chromosome = 3 Strand = positive ConnectronObjectNumber = 17163
US-10-227-567-1973

Query Match      65.0%; Score 13; DB 40; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCAGTTGAAG 15

RESULT 27
US-10-367-729A-1071/c
; Sequence 1071, Application US/10367729A
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; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,729A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1071
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 157
US-10-367-729A-1071

Query Match      65.0%; Score 13; DB 46; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 13 GCCCCAGTTGAAG 1
   |||||

RESULT 28
US-10-367-729A-1072
; Sequence 1072, Application US/10367729A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,729A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1072
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 156
US-10-367-729A-1072

Query Match      65.0%; Score 13; DB 46; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 13 GCCCCAGTTGAAG 1
   |||||

RESULT 29
US-10-367-729A-1973/c
; Sequence 1973, Application US/10367729A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,729A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1973
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 156
US-10-367-729A-1072

Query Match      65.0%; Score 13; DB 46; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 3 GCCCCAGTTGAAG 15
   |||||

RESULT 29
US-10-367-729A-1973/c
; Sequence 1973, Application US/10367729A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,729A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 1973
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (65988)...(66002)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 156
US-10-367-729A-1072

Query Match      65.0%; Score 13; DB 46; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 3 GCCCCAGTTGAAG 15
   |||||
```

```
; LOCATION: (2790547)...(2790562)
; OTHER INFORMATION: Chromosome = 3 Strand = positive ConnectronObjectNumber = 17163
US-10-367-729A-1973

Query Match      65.0%; Score 13; DB 46; Length 15;
Score over Length 86.7%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
   |||||
Db 13 GCCCCAGTTGAAG 1
   |||||

RESULT 30
US-10-708-953-550673/c
; Sequence 550673, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 550673
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-550673

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
   |||||
Db 12 GTTGAAGTTGCC 1
   |||||

RESULT 31
US-10-708-953-691520/c
; Sequence 691520, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 691520
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-691520

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
   |||||
Db 12 GTTGAAGTTGCC 1
   |||||

RESULT 32
US-10-708-953-1007429/c
; Sequence 1007429, Application US/10708953
```

```
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1007429
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1007429

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGATGTTGCC 1

RESULT 33
US-10-708-953-1161356/c
; Sequence 1161356, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1161356
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1161356

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGATGTTGCC 1

RESULT 34
US-10-708-953-1293526/c
; Sequence 1293526, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1293526
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1293526

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGATGTTGCC 1

RESULT 35
US-10-708-953-1483914/c
; Sequence 1483914, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1483914
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1483914

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGATGTTGCC 1

RESULT 36
US-10-708-953-1637846/c
; Sequence 1637846, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1637846
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1637846

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGATGTTGCC 1

RESULT 37
US-10-708-953-1982721/c
; Sequence 1982721, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
```

```
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGATGTTGCC 1

RESULT 35
US-10-708-953-1483914/c
; Sequence 1483914, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1483914
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1483914

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGATGTTGCC 1

RESULT 36
US-10-708-953-1637846/c
; Sequence 1637846, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1637846
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1637846

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGATGTTGCC 1

RESULT 37
US-10-708-953-1982721/c
; Sequence 1982721, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
```

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; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1982721
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1982721

Query Match      52.0%; Score 10.4; DB 52; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 38
US-10-708-953A-550673/c
; Sequence 550673, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 550673
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-550673

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 39
US-10-708-953A-691520/c
; Sequence 691520, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 691520
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-691520

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 40
US-10-708-953A-1007429/c
; Sequence 1007429, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1007429
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1007429

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 41
US-10-708-953A-1161356/c
; Sequence 1161356, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1161356
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1161356

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGATGTTGCC 1

RESULT 42
US-10-708-953A-1293526/c
; Sequence 1293526, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1293526
; LENGTH: 12
; TYPE: RNA
```

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; ORGANISM: Homo sapiens
US-10-708-953A-1293526

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
   ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 43
US-10-708-953A-1483914/c
; Sequence 1483914, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1483914
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1483914

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
   ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 44
US-10-708-953A-1637846/c
; Sequence 1637846, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1637846
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1637846

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
   ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 45
US-10-708-953A-1982721/c
; Sequence 1982721, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1982721
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1982721

Query Match      52.0%; Score 10.4; DB 53; Length 12;
Score over Length 86.7%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
   ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 46
PCT-US07-68401-1552/c
; Sequence 1552, Application PC/TUS0768401
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric B. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061US7
; CURRENT APPLICATION NUMBER: PCT/US07/68401
; CURRENT FILING DATE: 2007-05-25
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68401-1552

Query Match      60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
   ||||| |||||
Db 12 GTTGATGTTGCC 1

RESULT 47
```

PCT-US07-68403-1552/c  
; Sequence 1552, Application PC/TUS0768402  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wanczewicz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: CORE0061W015  
; CURRENT APPLICATION NUMBER: PCT/US07/68402  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1552  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68402-1552  
Query Match 60.0%; Score 12; DB 3; Length 14;  
Score over Length 85.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 7 GTTGAAGTTGCC 18  
Db 12 GTTGAAGTTGCC 1  
RESULT 48  
PCT-US07-68403-1552/c  
; Sequence 1552, Application PC/TUS0768403  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wanczewicz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: CORE0061W08  
; CURRENT APPLICATION NUMBER: PCT/US07/68403  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1552  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68402-1552  
Query Match 60.0%; Score 12; DB 3; Length 14;  
Score over Length 85.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 7 GTTGAAGTTGCC 18  
Db 12 GTTGAAGTTGCC 1  
RESULT 48  
PCT-US07-68403-1552/c  
; Sequence 1552, Application PC/TUS0768403  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wanczewicz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: CORE0061W08  
; CURRENT APPLICATION NUMBER: PCT/US07/68403  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23

; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1552  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68403-1552  
Query Match 60.0%; Score 12; DB 3; Length 14;  
Score over Length 85.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 7 GTTGAAGTTGCC 18  
Db 12 GTTGAAGTTGCC 1  
RESULT 49  
PCT-US07-68404-1552/c  
; Sequence 1552, Application PC/TUS0768404  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wanczewicz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: CORE0061W010  
; CURRENT APPLICATION NUMBER: PCT/US07/68404  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1552  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68404-1552  
Query Match 60.0%; Score 12; DB 3; Length 14;  
Score over Length 85.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 7 GTTGAAGTTGCC 18  
Db 12 GTTGAAGTTGCC 1  
RESULT 50  
PCT-US07-68406-1552/c  
; Sequence 1552, Application PC/TUS0768406

```
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W09
; CURRENT APPLICATION NUMBER: PCT/US07/68406
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68406-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 51
PCT-US07-68408-1552/c
; Sequence 1552, Application PC/TUS0768408
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W01
; CURRENT APPLICATION NUMBER: PCT/US07/68408
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68406-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 51
PCT-US07-68408-1552/c
; Sequence 1552, Application PC/TUS0768408
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W01
; CURRENT APPLICATION NUMBER: PCT/US07/68408
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
```

```
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68408-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 52
PCT-US07-68410-1552/c
; Sequence 1552, Application PC/TUS0768410
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061W012
; CURRENT APPLICATION NUMBER: PCT/US07/68410
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1552
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68410-1552

Query Match 60.0%; Score 12; DB 3; Length 14;
Score over Length 85.7%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGTTGCC 1

RESULT 53
PCT-US07-68412-1552/c
; Sequence 1552, Application PC/TUS0768412
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
```

APPLICANT: Sanjay Bhanot  
APPLICANT: Richard S. Geary  
APPLICANT: Robert McKay  
APPLICANT: Brett P. Monia  
APPLICANT: Punit P. Seth  
APPLICANT: Andrew M. Siwkowski  
APPLICANT: Eric E. Swayze  
APPLICANT: Edward Wancewitz  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
TITLE OF INVENTION: EXPRESSION OF GCGR  
FILE REFERENCE: CORE0061W013  
CURRENT APPLICATION NUMBER: PCT/US07/68412  
CURRENT FILING DATE: 2007-05-25  
PRIOR APPLICATION NUMBER: PCT/US2007/061183  
PRIOR FILING DATE: 2007-01-27  
PRIOR APPLICATION NUMBER: 60/746,631  
PRIOR FILING DATE: 2006-05-05  
PRIOR APPLICATION NUMBER: 60/747,059  
PRIOR FILING DATE: 2006-05-11  
PRIOR APPLICATION NUMBER: 60/805,660  
PRIOR FILING DATE: 2006-06-23  
PRIOR APPLICATION NUMBER: 60/864,554  
PRIOR FILING DATE: 2006-11-06  
NUMBER OF SEQ ID NOS: 1576  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1552  
LENGTH: 14  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68412-1552

Query Match 60.0%; Score 12; DB 3; Length 14;  
Score over Length 85.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18  
Db 12 GTTGAAGTTGCC 1

RESULT 54  
US-11-745-429-1552/c  
Sequence 1552, Application US/11745429  
GENERAL INFORMATION:  
APPLICANT: Sanjay Bhanot  
APPLICANT: Richard S. Geary  
APPLICANT: Robert McKay  
APPLICANT: Brett P. Monia  
APPLICANT: Punit P. Seth  
APPLICANT: Andrew M. Siwkowski  
APPLICANT: Eric E. Swayze  
APPLICANT: Edward Wancewitz  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
TITLE OF INVENTION: GENE EXPRESSION  
FILE REFERENCE: CORE0061US7  
CURRENT APPLICATION NUMBER: US/11745,429  
CURRENT FILING DATE: 2007-05-25  
PRIOR APPLICATION NUMBER: PCT/US2007/061183  
PRIOR FILING DATE: 2007-01-27  
PRIOR APPLICATION NUMBER: 60/746,631  
PRIOR FILING DATE: 2006-05-05  
PRIOR APPLICATION NUMBER: 60/747,059  
PRIOR FILING DATE: 2006-05-11  
PRIOR APPLICATION NUMBER: 60/805,660  
PRIOR FILING DATE: 2006-06-23  
PRIOR APPLICATION NUMBER: 60/864,554  
PRIOR FILING DATE: 2006-11-06  
NUMBER OF SEQ ID NOS: 1576  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1552

LENGTH: 14  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-11-745-429-1552

Query Match 60.0%; Score 12; DB 81; Length 14;  
Score over Length 85.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18  
Db 12 GTTGAAGTTGCC 1

RESULT 55  
PCT-US02-22417-5  
Sequence 5, Application PC/TUS0222417  
GENERAL INFORMATION:  
APPLICANT: Hong Zhang  
APPLICANT: Andrew T. Watt  
APPLICANT: Isis Pharmaceuticals, Inc.  
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
FILE REFERENCE: RTSP-0395  
CURRENT APPLICATION NUMBER: PCT/US02/22417  
CURRENT FILING DATE: 2002-07-13  
PRIOR APPLICATION NUMBER: 09/908,147  
PRIOR FILING DATE: 2001-07-17  
NUMBER OF SEQ ID NOS: 168  
SEQ ID NO 5  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR Primer  
PCT-US02-22417-5

Query Match 75.0%; Score 15; DB 1; Length 18;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAGTT 15  
Db 4 GCCCAGTTGAAGTT 18

RESULT 56  
US-09-908-147-5  
Sequence 5, Application US/09908147  
GENERAL INFORMATION:  
APPLICANT: Hong Zhang  
APPLICANT: Andrew T. Watt  
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
FILE REFERENCE: RTS-0185  
CURRENT APPLICATION NUMBER: US/09/908,147  
CURRENT FILING DATE: 2001-07-17  
NUMBER OF SEQ ID NOS: 168  
SEQ ID NO 5  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR Primer  
US-09-908-147-5

Query Match 75.0%; Score 15; DB 34; Length 18;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15  
|||||  
DB 4 GCCCCAGTTGAAGTT 18

## RESULT 57

US-10-728-509-5  
; Sequence 5, Application US/10728509  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-10-728-509-5

Query Match 75.0%; Score 15; DB 56; Length 18;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15  
|||||  
DB 4 GCCCCAGTTGAAGTT 18

## RESULT 58

US-10-257-017B-271773/c  
; Sequence 271773, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 271773  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002613  
US-10-257-017B-271773

Query Match 50.0%; Score 10; DB 40; Length 12;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
DB 10 AGTTGAAGTT 1

## RESULT 59

US-10-257-017B-274756/c  
; Sequence 274756, Application US/10257017B  
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 274756  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003668  
US-10-257-017B-274756

Query Match 50.0%; Score 10; DB 40; Length 12;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
DB 10 AGTTGAAGTT 1

## RESULT 60

US-10-257-017B-310208  
; Sequence 310208, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 310208  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023863  
US-10-257-017B-310208

Query Match 50.0%; Score 10; DB 40; Length 12;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
|||||  
DB 1 GTTGAAGTTG 10

## RESULT 61

US-10-257-017B-341473/c  
; Sequence 341473, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B



```
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341473
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042053
US-10-257-017B-341473

Query Match      50.0%; Score 10; DB 40; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTTGAAGTT 2

RESULT 62
US-10-257-017B-353251
; Sequence 353251, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353251
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048401
US-10-257-017B-353251

Query Match      50.0%; Score 10; DB 40; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 1 AGTTGAAGTT 10

RESULT 63
US-10-257-017B-355811/c
; Sequence 355811, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 355811
; LENGTH: 12
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049826
US-10-257-017B-355811

Query Match      50.0%; Score 10; DB 40; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1

RESULT 64
PCT-US02-22417-119
; Sequence 119, Application PC/TUS0222417
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTSP-0395
; CURRENT APPLICATION NUMBER: PCT/US02/22417
; CURRENT FILING DATE: 2002-07-13
; PRIOR APPLICATION NUMBER: 09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-22417-119

Query Match      82.0%; Score 16.4; DB 1; Length 20;
Score over Length 82.0%;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCCGT 20
Db 1 CCCAGTTGAAGTTGCCAT 18

RESULT 65
US-09-908-147-119
; Sequence 119, Application US/09908147
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-119

Query Match      82.0%; Score 16.4; DB 34; Length 20;
Score over Length 82.0%;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCCGT 20
Db 1 CCCAGTTGAAGTTGCCAT 18
```

Db 1 CCAGTTGAAGTTGCCAT 18

RESULT 66  
US-10-728-509-119  
; Sequence 119, Application US/10728509  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 119  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-728-509-119

Query Match 82.0%; Score 16.4; DB 56; Length 20;  
Score over Length 82.0%;  
Best Local Similarity 94.4%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCAGTTGAAGTTGCCGT 20  
|||||

Db 1 CCAGTTGAAGTTGCCAT 18  
|||||

RESULT 67  
US-08-591-486B-33  
; Sequence 33, Application US/08591486B  
; GENERAL INFORMATION:  
; APPLICANT: Schlengersiepen, Georg F  
; APPLICANT: Schlengersiepen, Reimar  
; APPLICANT: Schlengersiepen, Karl-Hermann  
; APPLICANT: Göttingen, Wolfgang Brysch  
; TITLE OF INVENTION: A Pharmaceutical Composition  
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatm  
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the  
; TITLE OF INVENTION: Treatment of Neoplasms  
; NUMBER OF SEQUENCES: 185  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh Street, N.W.  
; CITY: Washington, D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/591,486B  
; FILING DATE: 11-JAN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93111059.7  
; FILING DATE: 10-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP94/02218  
; FILING DATE: 6-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10496/P60122  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 393-9350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-08-591-486B-33

Query Match 57.0%; Score 11.4; DB 14; Length 14;  
Score over Length 81.4%;  
Best Local Similarity 92.3%; Pred. No. 7.8e+05;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19  
|||||

Db 2 GTTGAAGTTGCTG 14  
|||||

RESULT 68  
US-08-591-486C-33  
; Sequence 33, Application US/08591486C  
; GENERAL INFORMATION:  
; APPLICANT: Schlengersiepen, Georg F  
; APPLICANT: Schlengersiepen, Reimar  
; APPLICANT: Schlengersiepen, Karl-Hermann  
; APPLICANT: Göttingen, Wolfgang Brysch  
; TITLE OF INVENTION: A Pharmaceutical Composition Comprising Antisense-Nucleic Acid for  
; TITLE OF INVENTION: Prevention and/or Treatment of Neuronal Injury, Degeneration and  
; TITLE OF INVENTION: for the Treatment of Neoplasms  
; FILE REFERENCE: P60122  
; CURRENT APPLICATION NUMBER: US/08/591,486C  
; CURRENT FILING DATE: 1996-01-11  
; PRIOR APPLICATION NUMBER: PCT/EP94/02218  
; PRIOR FILING DATE: 1994-07-06  
; PRIOR APPLICATION NUMBER: EP 93111059.7  
; PRIOR FILING DATE: 1993-07-10  
; NUMBER OF SEQ ID NOS: 186  
; SEQ ID NO 33  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Antisense nucleic acid  
US-08-591-486C-33

Query Match 57.0%; Score 11.4; DB 14; Length 14;  
Score over Length 81.4%;  
Best Local Similarity 92.3%; Pred. No. 7.8e+05;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19  
|||||

Db 2 GTTGAAGTTGCTG 14  
|||||

RESULT 69  
US-10-708-953-393713  
; Sequence 393713, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 393713

```
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-393713

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 70
US-10-708-953-445749
; Sequence 445749, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 445749
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-445749

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 71
US-10-708-953-591846
; Sequence 591846, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 591846
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-591846

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 72
US-10-708-953-783771
; Sequence 783771, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 783771
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-783771

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 73
US-10-708-953-1022044
; Sequence 1022044, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1022044
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1022044

Query Match      57.0%; Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :|||
Db 2 GCCCCACUUGAAG 14

RESULT 74
US-10-708-953-1241906
; Sequence 1241906, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1241906
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1241906

Query Match      57.0%; Score 11.4; DB 52; Length 14;
```

```
Score over Length      81.4%;      Pred. No. 7.8e+05;
Best Local Similarity  76.9%;      2; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative

Qy 1 GCCCCAGTTGAAG 13
Db 2 GCCCCACUUGAAG 14

RESULT 75
US-10-708-953-1832566
; Sequence 1832566, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1832566
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1832566

Query Match      57.0%;      Score 11.4; DB 52; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 2 GCCCCACUUGAAG 14

RESULT 76
US-10-708-953A-393713
; Sequence 393713, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 393713
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-393713

Query Match      57.0%;      Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 2 GCCCCACUUGAAG 14

RESULT 77
US-10-708-953A-445749
; Sequence 445749, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
```

```
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 445749
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-445749

Query Match      57.0%;      Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 2 GCCCCACUUGAAG 14

RESULT 78
US-10-708-953A-591846
; Sequence 591846, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 591846
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-591846

Query Match      57.0%;      Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 2 GCCCCACUUGAAG 14

RESULT 79
US-10-708-953A-783771
; Sequence 783771, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 783771
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-783771

Query Match      57.0%;      Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%;      Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 2 GCCCCACUUGAAG 14
```

```
Db      2 GCCCCACUUGAAG 14

RESULT 80
US-10-708-953A-1022044
; Sequence 1022044, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1022044
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1022044

Query Match      57.0%; Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAAG 13
        ||||| :|||
Db      2 GCCCCACUUGAAG 14

RESULT 81
US-10-708-953A-1241906
; Sequence 1241906, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1241906
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1241906

Query Match      57.0%; Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAAG 13
        ||||| :|||
Db      2 GCCCCACUUGAAG 14

RESULT 82
US-10-708-953A-1832566
; Sequence 1832566, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1832566
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1832566

Query Match      57.0%; Score 11.4; DB 53; Length 14;
Score over Length 81.4%;
Best Local Similarity 76.9%; Pred. No. 7.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAAG 13
        ||||| :|||
Db      2 GCCCCACUUGAAG 14

RESULT 83
US-10-984-919-857
; Sequence 857, Application US/10984919
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 857
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-857

Query Match      57.0%; Score 11.4; DB 60; Length 14;
Score over Length 81.4%;
Best Local Similarity 92.3%; Pred. No. 7.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCCG 19
        ||||| :|||
Db      2 GTTGAAGTTGCTG 14

RESULT 84
US-10-594-448-16
; Sequence 16, Application US/10594448
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, Akira
; APPLICANT: OZAKI, Toshiro
; TITLE OF INVENTION: METHOD OF SCREENING COMPOUND CAPABLE OF ACCELERATING OR INHIBITING
; FILE REFERENCE: Q97365
; CURRENT APPLICATION NUMBER: US/10/594,448
; CURRENT FILING DATE: 2006-09-26
; PRIOR APPLICATION NUMBER: JP 2004-93,266
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: JP 2004-176,107
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
```

; OTHER INFORMATION: primer for Bax  
US-10-594-448-16

Query Match 80.0%; Score 16; DB 48; Length 20;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20  
|||||  
Db 1 CAGTTGAAGTTGCCGT 16

## RESULT 85

US-09-708-690-4126/c  
; Sequence 4126, Application US/09708690  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-L (400/002)  
; CURRENT APPLICATION NUMBER: US/09/708,690  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/594,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/685,664  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 20828  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4126  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-708-690-4126

Query Match 60.0%; Score 12; DB 30; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
Db 15 CCCAGTTGAAGT 4

## RESULT 86

US-09-870-161-4126/c  
; Sequence 4126, Application US/09870161  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-M (400/026)  
; CURRENT APPLICATION NUMBER: US/09/870,161  
; CURRENT FILING DATE: 2001-08-27  
; NUMBER OF SEQ ID NOS: 20821  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4126  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens

US-09-870-161-4126

Query Match 60.0%; Score 12; DB 33; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
Db 15 CCCAGTTGAAGT 4

## RESULT 87

US-10-287-949A-4126/c  
; Sequence 4126, Application US/10287949A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4126  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-4126

Query Match 60.0%; Score 12; DB 41; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
Db 15 CCCAGTTGAAGT 4

## RESULT 88

US-10-287-949B-4126/c  
; Sequence 4126, Application US/10287949B  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: 00-876-O (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949B  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 20824  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4126  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949B-4126

Query Match 60.0%; Score 12; DB 41; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||

```
Db      15 CCCAGTTGAAGT 4

RESULT 89
US-10-287-949C-4126/c
; Sequence 4126, Application US/10287949C
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 00-876-O (400/053)
; CURRENT APPLICATION NUMBER: US/10/287,949C
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 20824
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949C-4126

Query Match      60.0%; Score 12; DB 41; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAGT 14
      |||||
Db      15 CCCAGTTGAAGT 4

RESULT 90
US-10-294-038-5264/c
; Sequence 5264, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 5264
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (2313785)...(2313798)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6574
US-10-294-038-5264

Query Match      60.0%; Score 12; DB 41; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGC 17
      |||||
Db      15 AGTTGAAGTTGC 4

RESULT 91
US-10-294-038A-5264/c
; Sequence 5264, Application US/10294038A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038A
```

```
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 5264
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (2313785)...(2313798)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6574
US-10-294-038A-5264

Query Match      60.0%; Score 12; DB 41; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGC 17
      |||||
Db      15 AGTTGAAGTTGC 4

RESULT 92
US-10-951-303-4126/c
; Sequence 4126, Application US/10951303
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-4126

Query Match      60.0%; Score 12; DB 60; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAGT 14
      |||||
Db      15 CCCAGTTGAAGT 4

RESULT 93
US-10-951-303B-4126/c
; Sequence 4126, Application US/10951303B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions
; TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor
```

FILE REFERENCE: 400/158 (MBH00-876-P)  
CURRENT APPLICATION NUMBER: US/10/951.303B  
CURRENT FILING DATE: 2004-09-27  
PRIOR APPLICATION NUMBER: US 09/685,664  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
PRIOR APPLICATION NUMBER: US 09/371,772  
PRIOR FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8228  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4126  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-951-303B-4126

Query Match 60.0%; Score 12; DB 60; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
DB 15 CCCAGTTGAAGT 4

RESULT 94  
US-11-088-219-4126/c  
Sequence 4126, Application US/11088219  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or  
TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor  
TITLE OF INVENTION: (VEGF-R)  
FILE REFERENCE: MBH00-876-Q (400/266)  
CURRENT APPLICATION NUMBER: US/11/088,219  
CURRENT FILING DATE: 2005-03-23  
PRIOR APPLICATION NUMBER: 10/138,674  
PRIOR FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: 09/870,161  
PRIOR FILING DATE: 2001-05-29  
PRIOR APPLICATION NUMBER: 09/708,690  
PRIOR FILING DATE: 2000-11-07  
PRIOR APPLICATION NUMBER: 09/371,722  
PRIOR FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: 08/584,040  
PRIOR FILING DATE: 2002-02-12  
PRIOR APPLICATION NUMBER: 60/005,974  
PRIOR FILING DATE: 1995-10-26  
NUMBER OF SEQ ID NOS: 20829  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4126  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-088-219-4126

Query Match 60.0%; Score 12; DB 63; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
DB 15 CCCAGTTGAAGT 4

## RESULT 95

US-11-088-219A-4126/c  
Sequence 4126, Application US/11088219A  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan  
TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or  
TITLE OF INVENTION: Conditions  
TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: 400/266 (MBH00-876-Q)  
CURRENT APPLICATION NUMBER: US/11/088,219A  
CURRENT FILING DATE: 2005-03-23  
NUMBER OF SEQ ID NOS: 20829  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4126  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-088-219A-4126

Query Match 60.0%; Score 12; DB 63; Length 15;  
Score over Length 80.0%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
DB 15 CCCAGTTGAAGT 4

## RESULT 96

US-10-257-017B-187031  
Sequence 187031, Application US/10257017B  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
APPLICANT: Kurt Berlin  
TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
TITLE OF INVENTION: methylations  
FILE REFERENCE: E01/1193/WO  
CURRENT APPLICATION NUMBER: US/10/257,017B  
CURRENT FILING DATE: 2002-10-07  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 382046  
SEQ ID NO 187031  
LENGTH: 13  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102  
US-10-257-017B-187031

Query Match 52.0%; Score 10.4; DB 40; Length 13;  
Score over Length 80.0%;  
Best Local Similarity 91.7%; Pred. No. 2.5e+06;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17  
|||||  
DB 1 AGTTGAAGTTGC 12

## RESULT 97

US-10-257-017B-187032/c  
Sequence 187032, Application US/10257017B  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock



```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187032
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187032

Query Match      52.0%; Score 10.4; DB 40; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTGCGCT 17
Db      13 AGTTGAAGTTGCGC 2

RESULT 98
PCT-US06-29646A-94101
; Sequence 94101, Application PC/TUS0629646A
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAs AND METHODS OF USE
; FILE REFERENCE: 99689-00009
; CURRENT APPLICATION NUMBER: PCT/US06/29646A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94101
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
PCT-US06-29646A-94101

Query Match      67.0%; Score 13.4; DB 3; Length 17;
Score over Length 78.8%;
Best Local Similarity 93.3%; Pred. No. 7.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTGCGCT 20
Db      3 AGTTGAAGTTGCGCT 17

RESULT 99
PCT-US06-29646A-94101
; Sequence 94101, Application US/11495951A
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAs AND METHODS OF USE
; FILE REFERENCE: 99689-00009
```

```
; CURRENT APPLICATION NUMBER: US/11/495,951A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94101
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-495-951A-94101
```

```
Query Match      67.0%; Score 13.4; DB 77; Length 17;
Score over Length 78.8%;
Best Local Similarity 93.3%; Pred. No. 7.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTGCGCT 20
Db      3 AGTTGAAGTTGCGCT 17
```

```
RESULT 100
PCT-US07-68401-1116/c
; Sequence 1116, Application PC/TUS0768401
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancowitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061157
; CURRENT APPLICATION NUMBER: PCT/US07/68401
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68401-1116
```

```
Query Match      47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      12 AGTTGAAGTTG 2

RESULT 101
```

PCT-US07-68402-1116/c  
; Sequence 1116, Application PC/TUS0768402  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wanczewitz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: CORE0061W015  
; CURRENT APPLICATION NUMBER: PCT/US07/68402  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1116  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68402-1116  
  
Query Match 47.0%; Score 9.4; DB 3; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 6 AGTTGAAGTTG 16  
| | | | | | | | | | | | | | | |  
Db 12 AGTTGGAGTTG 2  
  
RESULT 102  
PCT-US07-68403-1116/c  
; Sequence 1116, Application PC/TUS0768403  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wanczewitz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: CORE0061W08  
; CURRENT APPLICATION NUMBER: PCT/US07/68403  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23

; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1116  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68403-1116  
  
Query Match 47.0%; Score 9.4; DB 3; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 6 AGTTGAAGTTG 16  
| | | | | | | | | | | | | | | |  
Db 12 AGTTGGAGTTG 2  
  
RESULT 103  
PCT-US07-68404-1116/c  
; Sequence 1116, Application PC/TUS0768404  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wanczewitz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: CORE0061W010  
; CURRENT APPLICATION NUMBER: PCT/US07/68404  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1116  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68404-1116  
  
Query Match 47.0%; Score 9.4; DB 3; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 6 AGTTGAAGTTG 16  
| | | | | | | | | | | | | | | |  
Db 12 AGTTGGAGTTG 2  
  
RESULT 104  
PCT-US07-68406-1116/c  
; Sequence 1116, Application PC/TUS0768406

```
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punith P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF SGLT2
; FILE REFERENCE: CORE0061W09
; CURRENT APPLICATION NUMBER: PCT/US07/68406
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68406-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGGAGTTG 2

RESULT 105
PCT-US07-68408-1116/c
; Sequence 1116, Application PC/TUS0768408
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punith P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF CRP
; FILE REFERENCE: CORE0061W011
; CURRENT APPLICATION NUMBER: PCT/US07/68408
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68408-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGGAGTTG 2
```

```
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punith P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: EXPRESSION OF GCCR
; FILE REFERENCE: CORE0061W012
; CURRENT APPLICATION NUMBER: PCT/US07/68410
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68410-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGGAGTTG 2

RESULT 107
PCT-US07-68412-1116/c
; Sequence 1116, Application PC/TUS0768412
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
```

APPLICANT: Sanjay Bhanot  
APPLICANT: Richard S. Geary  
APPLICANT: Robert McKay  
APPLICANT: Brett P. Monia  
APPLICANT: Punit P. Seth  
APPLICANT: Andrew M. Siwkowski  
APPLICANT: Eric E. Swayze  
APPLICANT: Edward Wanczewitz  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
TITLE OF INVENTION: EXPRESSION OF GCCR  
FILE REFERENCE: CORE061W013  
CURRENT APPLICATION NUMBER: PCT/US07/68412  
CURRENT FILING DATE: 2007-05-25  
PRIOR APPLICATION NUMBER: PCT/US2007/061183  
PRIOR FILING DATE: 2007-01-27  
PRIOR APPLICATION NUMBER: 60/746,631  
PRIOR FILING DATE: 2006-05-05  
PRIOR APPLICATION NUMBER: 60/747,059  
PRIOR FILING DATE: 2006-05-11  
PRIOR APPLICATION NUMBER: 60/805,660  
PRIOR FILING DATE: 2006-06-23  
PRIOR APPLICATION NUMBER: 60/864,554  
PRIOR FILING DATE: 2006-11-06  
NUMBER OF SEQ ID NOS: 1576  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1116  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68412-1116

Query Match 47.0%; Score 9.4; DB 3; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 6 AGTTGAAGTTG 16  
Db 12 AGTTGAAGTTG 2

RESULT 108  
PCT-US98-26935-370/c  
Sequence 370, Application PC/TUS9826935  
GENERAL INFORMATION:  
APPLICANT: Jessen, Holly  
APPLICANT: Webb, David  
APPLICANT: Coryell, Virginia H.  
APPLICANT: Schupp, James M.  
APPLICANT: Keim, Paul S.  
APPLICANT: Pioneer Hi-Bred International, Inc.  
TITLE OF INVENTION: Nucleotide Polymorphisms in Soybean  
FILE REFERENCE: 018574-000110PC  
CURRENT APPLICATION NUMBER: PCT/US98/26935  
CURRENT FILING DATE: 1998-12-18  
EARLIER APPLICATION NUMBER: US 60/068,185  
EARLIER FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 795  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 370  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Glycine max  
PCT-US98-26935-370

Query Match 47.0%; Score 9.4; DB 3; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 4 CCAGTTGAAGT 14

Db 11 CCAGTTGAAGT 1

RESULT 109  
US-09-215-436-370/c  
Sequence 370, Application US/09215436  
GENERAL INFORMATION:  
APPLICANT: Jessen, Holly  
APPLICANT: Webb, David  
APPLICANT: Coryell, Virginia H.  
APPLICANT: Schupp, James M.  
APPLICANT: Keim, Paul S.  
APPLICANT: Pioneer Hi-Bred International, Inc.  
TITLE OF INVENTION: Nucleotide Polymorphisms in Soybean  
FILE REFERENCE: 018574-000110US  
CURRENT APPLICATION NUMBER: US/09/215,436  
CURRENT FILING DATE: 1998-12-18  
EARLIER APPLICATION NUMBER: US 60/068,185  
EARLIER FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 795  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 370  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Glycine max  
US-09-215-436-370

Query Match 47.0%; Score 9.4; DB 21; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
Db 11 CCAGTTGAAGT 1

RESULT 110  
US-09-581-970A-370/c  
Sequence 370, Application US/09581970A  
GENERAL INFORMATION:  
APPLICANT: Jessen, Holly  
APPLICANT: Webb, David  
APPLICANT: Coryell, Virginia H.  
APPLICANT: Schupp, James M.  
APPLICANT: Keim, Paul S.  
APPLICANT: Pioneer Hi-Bred International, Inc.  
TITLE OF INVENTION: Nucleotide Polymorphisms in Soybean  
FILE REFERENCE: 04-000111US  
CURRENT APPLICATION NUMBER: US/09/581,970A  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: PCT/US98/26935  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: 60/068,185  
PRIOR FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 798  
SOFTWARE: PatentIn Ver 2.1  
SEQ ID NO 370  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Glycine max  
US-09-581-970A-370

Query Match 47.0%; Score 9.4; DB 26; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
Db 11 CCAGTTGAAGT 1

```
RESULT 111
US-10-257-017B-275133/c
; Sequence 275133, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 275133
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003795
US-10-257-017B-275133

Query Match      47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGAGTTG 2

RESULT 112
US-10-257-017B-280261
; Sequence 280261, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 280261
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008409
US-10-257-017B-280261

Query Match      47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 6 AGTTGAAGTTG 16
Db 1 AGTTGAAGTTG 11

RESULT 113
US-10-257-017B-281972/c
; Sequence 281972, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
```

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281972
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010216
US-10-257-017B-281972

Query Match      47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 6 AGTTGAAGTTG 16
Db 11 AGTTGTAGTTG 1

RESULT 114
US-10-257-017B-282569/c
; Sequence 282569, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 282569
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010870
US-10-257-017B-282569

Query Match      47.0%; Score 9.4; DB 40; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTTGTAGTTG 2

RESULT 115
US-10-257-017B-300630
; Sequence 300630, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 300630  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019120  
US-10-257-017B-300630

Query Match 47.0%; Score 9.4; DB 40; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 2 AGTTGAAGTTG 12

## RESULT 116

US-10-257-017B-305246  
; Sequence 305246, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methyations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 305246  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021354  
US-10-257-017B-305246

Query Match 47.0%; Score 9.4; DB 40; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 2 AGTTGATGTTG 12

## RESULT 117

US-10-257-017B-314348  
; Sequence 314348, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methyations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 314348  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026294  
US-10-257-017B-314348

Query Match 47.0%; Score 9.4; DB 40; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-257-017B-314348

Query Match 47.0%; Score 9.4; DB 40; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 2 AGTTAAAGTTG 12

## RESULT 118

US-10-257-017B-329434  
; Sequence 329434, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methyations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 329434  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034943  
US-10-257-017B-329434

Query Match 47.0%; Score 9.4; DB 40; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 1 AGTAGAAGTTG 11

## RESULT 119

US-10-257-017B-337757  
; Sequence 337757, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methyations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 337757  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004732  
US-10-257-017B-337757

Query Match 47.0%; Score 9.4; DB 40; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
Db 1 AGTGAAGTTG 11

RESULT 120  
US-10-257-017B-339358/c  
; Sequence 339358, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 339358  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040958  
US-10-257-017B-339358

Query Match 47.0%; Score 9.4; DB 40; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
Db 11 AATTGAAGTTG 1

RESULT 121  
US-10-257-017B-345090/c  
; Sequence 345090, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 345090  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043868  
US-10-257-017B-345090

Query Match 47.0%; Score 9.4; DB 40; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
Db 11 AGTTGAGTTG 1

RESULT 122  
US-10-257-017B-361423

; Sequence 361423, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 361423  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052630  
US-10-257-017B-361423

Query Match 47.0%; Score 9.4; DB 40; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 90.9%; Pred. No. 8e+06; Indels 1; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
Db 1 AGTTGAAGTTG 11

RESULT 123  
US-10-708-952A-226611  
; Sequence 226611, Application US/10708952A  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL  
; FILE REFERENCE: 55035  
; CURRENT APPLICATION NUMBER: US/10/708,952A  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 399737  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 226611  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: JC virus  
US-10-708-952A-226611

Query Match 47.0%; Score 9.4; DB 51; Length 12;  
Score over Length 78.3%;  
Best Local Similarity 54.5%; Pred. No. 8e+06; Indels 1; Gaps 0;  
Matches 6; Conservative 4; Mismatches 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTT 15  
Db 1 CAGUUGCAGUU 11

RESULT 124  
US-10-708-952A-365157  
; Sequence 365157, Application US/10708952A  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL  
; FILE REFERENCE: 55035  
; CURRENT APPLICATION NUMBER: US/10/708,952A  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 399737  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 365157  
; LENGTH: 12

```
; TYPE: RNA
; ORGANISM: JC virus
US-10-708-952A-365157

Query Match      47.0%; Score 9.4; DB 51; Length 12;
Score over Length 78.3%;
Best Local Similarity 54.5%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 6; Conservative 4; Mismatches 1;

QY 5 CAGTTGAAGTT 15
   |||::|||::
Db 1 CAGUUGCAGU 11

RESULT 125
US-10-708-952B-226611
; Sequence 226611, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 226611
; LENGTH: 12
; TYPE: RNA
; ORGANISM: JC virus
US-10-708-952B-226611

Query Match      47.0%; Score 9.4; DB 51; Length 12;
Score over Length 78.3%;
Best Local Similarity 54.5%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 6; Conservative 4; Mismatches 1;

QY 5 CAGTTGAAGTT 15
   |||::|||::
Db 1 CAGUUGCAGU 11

RESULT 126
US-10-708-952B-365157
; Sequence 365157, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 365157
; LENGTH: 12
; TYPE: RNA
; ORGANISM: JC virus
US-10-708-952B-365157

Query Match      47.0%; Score 9.4; DB 51; Length 12;
Score over Length 78.3%;
Best Local Similarity 54.5%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 6; Conservative 4; Mismatches 1;

QY 5 CAGTTGAAGTT 15
   |||::|||::
Db 1 CAGUUGCAGU 11

RESULT 127
US-10-708-952B-365157
; Sequence 365157, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 365157
; LENGTH: 12
; TYPE: RNA
; ORGANISM: JC virus
US-10-708-952B-365157

Query Match      47.0%; Score 9.4; DB 51; Length 12;
Score over Length 78.3%;
Best Local Similarity 54.5%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 6; Conservative 4; Mismatches 1;

QY 5 CAGTTGAAGTT 15
   |||::|||::
Db 1 CAGUUGCAGU 11

RESULT 128
US-10-708-953-675075
; Sequence 675075, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 675075
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-675075

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12

RESULT 129
US-10-708-953-820071
; Sequence 820071, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 820071
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-820071

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12
```

```
US-10-708-953-425654
; Sequence 425654, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 425654
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-425654

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12

RESULT 128
US-10-708-953-675075
; Sequence 675075, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 675075
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-675075

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12

RESULT 129
US-10-708-953-820071
; Sequence 820071, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 820071
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-820071

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCCAGTTGA 11
   |||::|||::
Db 2 GCCCCAGCUGA 12
```



```
Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCAGTTGA 11
DB 2 GCCCAGCUGA 12

RESULT 130
US-10-708-953-1049802
; Sequence 1049802, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1049802
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1049802

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCAGTTGA 11
DB 2 GCCCAGCUGA 12

RESULT 131
US-10-708-953-1146690/c
; Sequence 1146690, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1146690
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1146690

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCAGTTGA 11
DB 2 GCCCAGCUGA 12

RESULT 132
US-10-708-953-1160477/c
; Sequence 1160477, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1160477
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1160477

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCAGTTGA 11
DB 2 GCCCAGCUGA 12

RESULT 133
US-10-708-953-1217858/c
; Sequence 1217858, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1217858
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1217858

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCAGTTGA 11
DB 2 GCCCAGCUGA 12

RESULT 134
US-10-708-953-1458682/c
; Sequence 1458682, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1458682
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1458682

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 GCCCAGTTGA 11
DB 2 GCCCAGCUGA 12
```

```
FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1160477
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1160477

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 6 AGTTGAAGTTG 16
DB 11 AGTTGACAGTTG 1

RESULT 133
US-10-708-953-1217858/c
; Sequence 1217858, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1217858
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1217858

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 4 CCAGTTGAAGT 14
DB 12 CCAGATGAAGT 2

RESULT 134
US-10-708-953-1458682/c
; Sequence 1458682, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1458682
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1458682

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 4 CCAGTTGAAGT 14
DB 12 CCAGATGAAGT 2
```

```
Db      12 CCAGATGAAGT 2
||||| |||||
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2131356

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCAGTTGAAGT 14
||||| |||||
Db      12 CCAGATGAAGT 2
||||| |||||

RESULT 138
US-10-708-953-2226422/c
; Sequence 2226422, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2226422
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2226422

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTGC 17
||||| |||||
Db      12 GTTCAAGTTGC 2
||||| |||||

RESULT 139
US-10-708-953A-425654
; Sequence 425654, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 425654
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-425654

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTGA 11
||||| :||
Db      2 GCCCCAGCUGA 12
||||| :||

RESULT 140
US-10-708-953A-675075

Db      12 CCAGATGAAGT 2
||||| |||||
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2131356

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTGA 11
||||| :||
Db      2 GCCCCAGCUGA 12
||||| :||

RESULT 136
US-10-708-953-2110468/c
; Sequence 2110468, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2110468
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2110468

Query Match      47.0%; Score 9.4; DB 52; Length 12;
Score over Length 78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCCCAGTTGA 11
||||| :||
Db      2 GCCCCAGCUGA 12
||||| :||

RESULT 137
US-10-708-953-2131356/c
; Sequence 2131356, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2131356
```

```
; Sequence 675075, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 675075
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-675075

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGA 11
Db 2 GCCCCAGCUGA 12

RESULT 141
US-10-708-953A-820071
; Sequence 820071, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 820071
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-820071

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGA 11
Db 2 GCCCCAGCUGA 12

RESULT 142
US-10-708-953A-1049802
; Sequence 1049802, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1049802
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1049802

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 81.8%; Pred. No. 8e+06;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGA 11
Db 2 GCCCCAGCUGA 12

RESULT 143
US-10-708-953A-1146690/c
; Sequence 1146690, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1146690
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1146690

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTCAAGTTGC 17
Db 12 GTTCAAGTTGC 2

RESULT 144
US-10-708-953A-1160477/c
; Sequence 1160477, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1160477
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1160477

Query Match          47.0%; Score 9.4; DB 53; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 11 AGTTGAAGTTG 1

RESULT 145
US-10-708-953A-1217858/c
; Sequence 1217858, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
```

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; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1217858
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1217858

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
   ||||| |||||
Db 12 CCAGATGAAGT 2

RESULT 146
US-10-708-953A-1458682/c
; Sequence 1458682, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1458682
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1458682

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
   ||||| |||||
Db 12 CCAGATGAAGT 2

RESULT 147
US-10-708-953A-2070413
; Sequence 2070413, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2070413
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2070413

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
   ||||| |||||
Db 12 CCAGATGAAGT 2

RESULT 148
US-10-708-953A-2110468/c
; Sequence 2110468, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2110468
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2110468

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   ||||| |||||
Db 11 AGTTGCGAGTTG 1

RESULT 149
US-10-708-953A-2131356/c
; Sequence 2131356, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2131356
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2131356

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
   ||||| |||||
Db 12 CCAGATGAAGT 2

RESULT 150
US-10-708-953A-2226422/c
; Sequence 2226422, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2226422
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2226422

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14
   ||||| |||||
Db 12 CCAGATGAAGT 2
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2226422

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGC 17
   ||| |||||
Db 12 GTTCAAGTTGC 2

RESULT 151
US-10-709-572-155258
; Sequence 155258, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 155258
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-155258

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   ||| |||||
Db 1 ACTTGAAGTTG 11

RESULT 152
US-10-709-572-186135
; Sequence 186135, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 186135
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-186135

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   ||| |||||
Db 2 ACTTGAAGTTG 12

RESULT 153
US-10-709-572-269838
; Sequence 269838, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 269838
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-269838

Query Match      47.0%; Score 9.4; DB 53; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTT 15
   ||| |||||
Db 2 CTGTTGAAGTT 12

RESULT 154
US-11-745-429-1116/c
; Sequence 1116, Application US/11745429
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wancewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061US7
; CURRENT APPLICATION NUMBER: US/11/745,429
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-11-745-429-1116

Query Match      47.0%; Score 9.4; DB 81; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 8e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 6 AGTTGAAGTTG 16  
|||||  
Db 12 AGTTGAAGTTG 2

## RESULT 155

PCT-US02-25943-54229  
; Sequence 54229, Application PC/TUS0225943  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: PCT/US02/25943  
; CURRENT FILING DATE: 2002-08-27

; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 54229  
; LENGTH: 16

; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:

; LOCATION: (5299838)...(5299853)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 58096  
PCT-US02-25943-54229

Query Match 62.0%; Score 12.4; DB 1; Length 16;  
Score over Length 77.5%;  
Best Local Similarity 92.9%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20  
|||||  
Db 1 GGTGAAGTTGCCGT 14

## RESULT 156

US-10-227-565-54229  
; Sequence 54229, Application US/10227565  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/227,565  
; CURRENT FILING DATE: 2002-08-26

; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 54229  
; LENGTH: 16

; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:

; LOCATION: (5299838)...(5299853)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 58096  
US-10-227-565-54229

Query Match 62.0%; Score 12.4; DB 40; Length 16;  
Score over Length 77.5%;  
Best Local Similarity 92.9%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20  
|||||  
Db 1 GGTGAAGTTGCCGT 14

## RESULT 157

US-10-367-832A-54229  
; Sequence 54229, Application US/10367832A  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/367,832A

; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 54229  
; LENGTH: 16

; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:

; LOCATION: (5299838)...(5299853)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 58096  
US-10-367-832A-54229

Query Match 62.0%; Score 12.4; DB 46; Length 16;  
Score over Length 77.5%;  
Best Local Similarity 92.9%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20  
|||||  
Db 1 GGTGAAGTTGCCGT 14

## RESULT 158

US-10-471-899-5/c

; Sequence 5, Application US/10471899  
; GENERAL INFORMATION:

; APPLICANT: Diamond, Michael P.  
; TITLE OF INVENTION: METHOD OF PREVENTING ADHESIONS BY APOPTOSIS OF ADHESION  
; FILE REFERENCE: PERITONEAL CELLS  
; CURRENT APPLICATION NUMBER: US/10/471,899

; CURRENT FILING DATE: 2004-03-01  
; PRIOR APPLICATION NUMBER: PCT/US02/07119  
; PRIOR FILING DATE: 2002-03-11

; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.4

; SEQ ID NO 5  
; LENGTH: 22

; TYPE: DNA  
; ORGANISM: Homo Sapiens

US-10-471-899-5

Query Match 85.0%; Score 17; DB 47; Length 22;  
Score over Length 77.3%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGCCGT 20  
|||||  
Db 22 CCAGTTGAAGTTGCCGT 6

## RESULT 159

US-10-708-953-528084/c

; Sequence 528084, Application US/10708953  
; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: OLIGONUCLEOTIDES AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 528084  
; LENGTH: 14

; TYPE: RNA  
; ORGANISM: Homo sapiens

US-10-708-953-528084

Query Match 54.0%; Score 10.8; DB 52; Length 14;  
Score over Length 77.1%;

```
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCC 18
Db 14 CAGGTGAAGGTGCC 1

RESULT 160
US-10-708-953-613923
; Sequence 613923, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 613923
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-613923

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCGT 20
Db 1 GUUGAAGUGGCAU 14

RESULT 161
US-10-708-953-668724
; Sequence 668724, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 668724
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-668724

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGT 14
Db 1 GCCCAAGUGGCAU 14

RESULT 162
US-10-708-953-1269719/c
; Sequence 1269719, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
```

```
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1269719
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1269719

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCC 18
Db 14 CAGGTGAAGGTGCC 1

RESULT 163
US-10-708-953-1475347/c
; Sequence 1475347, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1475347
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1475347

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCC 18
Db 14 CAGGTGAAGGTGCC 1

RESULT 164
US-10-708-953-1713144/c
; Sequence 1713144, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1713144
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1713144

Query Match 54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCC 18
Db 14 CAGGTGAAGGTGCC 1
```

```
RESULT 165
US-10-708-953-1883139
; Sequence 1883139, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1883139
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1883139

Query Match      54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAAGT 14
DB 1 GCCCAGUUGCAGU 14

RESULT 166
US-10-708-953-1898598
; Sequence 1898598, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1898598
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1898598

Query Match      54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAAGT 14
DB 1 GCCCAGUUGCAGU 14

RESULT 167
US-10-708-953-2077386/c
; Sequence 2077386, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2077386
; LENGTH: 14
; TYPE: RNA
US-10-708-953-2077386/c

Query Match      54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
DB 1 GUUGAAGGUGGCCAU 14

RESULT 168
US-10-708-953A-528084/c
; Sequence 528084, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 528084
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-528084

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
DB 14 CAGGTGAAGTGCC 1

RESULT 169
US-10-708-953A-613923
; Sequence 613923, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 613923
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-613923

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
DB 14 CAGGTGAAGTGCC 1

RESULT 170
US-10-708-953A-668724
; Sequence 668724, Application US/10708953A
; GENERAL INFORMATION:
```

```
; ORGANISM: Homo sapiens
US-10-708-953-2077386
```

```
Query Match      54.0%; Score 10.8; DB 52; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
DB 14 CAGGTGAAGTGCC 1
```

```
RESULT 168
US-10-708-953A-528084/c
; Sequence 528084, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 528084
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-528084
```

```
Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
DB 14 CAGGTGAAGTGCC 1
```

```
RESULT 169
US-10-708-953A-613923
; Sequence 613923, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 613923
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-613923
```

```
Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20
DB 1 GUUGAAGGUGGCCAU 14
```

```
RESULT 170
US-10-708-953A-668724
; Sequence 668724, Application US/10708953A
; GENERAL INFORMATION:
```



```
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 668724
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-668724

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGT 14
   |||||:::|
Db 1 GCCCAAGUUGCAGU 14

RESULT 171
US-10-708-953A-1269719/c
; Sequence 1269719, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1269719
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1269719

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   |||||:::|
Db 14 CAGGTGAAGTGCC 14

RESULT 172
US-10-708-953A-1475347/c
; Sequence 1475347, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1475347
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1475347

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   |||||:::|
Db 14 CAGGTGAAGTGCC 14

RESULT 173
US-10-708-953A-1898598
; Sequence 1898598, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1898598
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1898598

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   |||||:::|
Db 14 CAGGTGAAGTGCC 14
```

```
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   |||||:::|
Db 14 CAGGTGAAGTGCC 14

RESULT 173
US-10-708-953A-1713144/c
; Sequence 1713144, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1713144
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1713144

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
   |||||:::|
Db 14 CAGGTGAAGTGCC 14

RESULT 174
US-10-708-953A-1883139
; Sequence 1883139, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1883139
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1883139

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 64.3%; Pred. No. 1.6e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGT 14
   |||||:::|
Db 1 GCCCAAGUUGCAGU 14

RESULT 175
US-10-708-953A-1998598
; Sequence 1998598, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
```

```
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1898598
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1898598

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCGCT 20
|:|||||:|:|:|
Db 1 GUUGAAGGUGCCAU 14

RESULT 176
US-10-708-953A-2077386/c
; Sequence 2077386, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2077386
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2077386

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCC 18
|||||
Db 14 CAGTGAAGTGCC 1

RESULT 177
US-10-709-572-163869/c
; Sequence 163869, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 163869
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-163869

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCG 19
|||||
Db 14 AGTTGAAGTTGCTG 1

RESULT 178
US-10-709-572-191117/c
; Sequence 191117, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191117
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-191117

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTT 15
|||||
Db 14 CCCCTGCTGAAGTT 1

RESULT 179
US-10-709-572-191263/c
; Sequence 191263, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191263
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-191263

Query Match      54.0%; Score 10.8; DB 53; Length 14;
Score over Length 77.1%;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTG 16
|||||
Db 14 CCCTGCTGAAGTTG 1

RESULT 180
US-10-709-572-276392/c
; Sequence 276392, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
```

; CURRENT APPLICATION NUMBER: US/10/709,572  
; CURRENT FILING DATE: 2005-05-14  
; NUMBER OF SEQ ID NOS: 10068324  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 276392  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-709-572-276392

Query Match 54.0%; Score 10.8; DB 53; Length 14;  
Score over Length 77.1%;  
Best Local Similarity 85.7%; Pred. No. 1.6e+06;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTCCCG 19  
Db 14 AGTTGAAGTTGCTG 1

RESULT 181  
PCT-US04-02720-1484/c  
; Sequence 1484, Application PC/TUS0402720  
; GENERAL INFORMATION:  
; APPLICANT: Keck Graduate Institute  
; APPLICANT: Van Ness, Jeffrey  
; APPLICANT: Galas, David J.  
; APPLICANT: Van Ness, Lori K.  
; TITLE OF INVENTION: ORGANISM FINGERPRINTING USING NICKING  
; FILE REFERENCE: 480188.422PC  
; CURRENT APPLICATION NUMBER: PCT/US04/02720  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 1817  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1484  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amplification product  
; NAME/KEY: misc\_feature  
; LOCATION: 7  
; OTHER INFORMATION: n = A,T,C or G  
PCT-US04-02720-1484

Query Match 50.0%; Score 10; DB 2; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 90.9%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13  
Db 13 CCCAGTGAAG 3

RESULT 182  
US-09-528-209A-6286  
; Sequence 6286, Application US/09528209A  
; GENERAL INFORMATION:  
; APPLICANT: Agilent Technologies  
; TITLE OF INVENTION: Computational Method for Constructing a Universal  
; TITLE OF INVENTION: Tag-Antitag Molecular Array System for Hybridization  
; TITLE OF INVENTION: Analysis  
; FILE REFERENCE: 10992790  
; CURRENT APPLICATION NUMBER: US/09/528,209A  
; CURRENT FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 10286  
; SOFTWARE: Bergetrom Sequence Formatter  
; SEQ ID NO 6286  
; LENGTH: 13  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A tag sequence incorporated in a probe nucleotide, the tag  
; OTHER INFORMATION: sequence complementary to an antitag sequence incorporated  
; OTHER INFORMATION: within a universal tag-antitag molecular array  
US-09-528-209A-6286

Query Match 50.0%; Score 10; DB 24; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16  
Db 4 GTTGAAGTTG 13

RESULT 183  
US-10-051-645B-5965  
; Sequence 5965, Application US/10051645B  
; GENERAL INFORMATION:  
; APPLICANT: Compugen Ltd  
; TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and  
; TITLE OF INVENTION: Methods of use thereof for Diagnosis  
; FILE REFERENCE: 1847.1009  
; CURRENT APPLICATION NUMBER: US/10/051,645B  
; CURRENT FILING DATE: 2005-01-27  
; NUMBER OF SEQ ID NOS: 6908  
; SEQ ID NO 5965  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-051-645B-5965

Query Match 50.0%; Score 10; DB 38; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16  
Db 3 GTTGAAGTTG 12

RESULT 184  
US-10-257-017B-28743  
; Sequence 28743, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 28743  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008356  
US-10-257-017B-28743

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 1 AGTTGAAGTT 10

## RESULT 185

US-10-257-017B-28744/c  
; Sequence 28744, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 28744  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008356  
US-10-257-017B-28744

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 13 AGTTGAAGTT 4

## RESULT 186

US-10-257-017B-65609  
; Sequence 65609, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 65609  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017271  
US-10-257-017B-65609

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 4 AGTTGAAGTT 13

## RESULT 187

US-10-257-017B-65610/c

US-10-257-017B-65610/c  
; Sequence 65610, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 65610  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017271  
US-10-257-017B-65610

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 10 AGTTGAAGTT 1

## RESULT 188

US-10-257-017B-107775  
; Sequence 107775, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 107775  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026982  
US-10-257-017B-107775

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 3 AGTTGAAGTT 12

## RESULT 189

US-10-257-017B-107776/c  
; Sequence 107776, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 107776
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026982
US-10-257-017B-10776

Query Match      50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
DB      11 AGTTGAAGTT 2

RESULT 190
US-10-257-017B-131257
; Sequence 131257, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131257
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032754
US-10-257-017B-131257

Query Match      50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
DB      1 GTTGAAGTTG 10

RESULT 191
US-10-257-017B-131258/c
; Sequence 131258, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 131258
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032754
US-10-257-017B-131258

Query Match      50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
DB      13 GTTGAAGTTG 4

RESULT 192
US-10-257-017B-150111
; Sequence 150111, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 150111
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037893
US-10-257-017B-150111

Query Match      50.0%; Score 10; DB 40; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
DB      4 AGTTGAAGTT 13

RESULT 193
US-10-257-017B-150112/c
; Sequence 150112, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 150112
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037893
US-10-257-017B-150112
```

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
|||||  
Db 10 AGTTGAAGTT 1

RESULT 194  
US-10-257-017B-153411  
; Sequence 153411, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 153411  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038780  
US-10-257-017B-153411

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 83.3%; Pred. No. 4e+06;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17  
|||||  
Db 2 AGTTGAAGATGY 13

RESULT 195  
US-10-257-017B-153412/c  
; Sequence 153412, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 153412  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038780  
US-10-257-017B-153412

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 83.3%; Pred. No. 4e+06;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17

Db 12 AGTTGAAGATGY 1  
|||||

RESULT 196  
US-10-257-017B-171651  
; Sequence 171651, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 171651  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042787  
US-10-257-017B-171651

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
|||||  
Db 2 AGTTGAAGTT 11

RESULT 197  
US-10-257-017B-171652/c  
; Sequence 171652, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 171652  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042787  
US-10-257-017B-171652

Query Match 50.0%; Score 10; DB 40; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 4e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
|||||  
Db 12 AGTTGAAGTT 3

RESULT 198  
US-11-043-842-704  
; Sequence 704, Application US/11043842

```

Query Match          50.0%; Score 10; DB 81; Length 13;
Score over Length    76.9%;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 3 GTTGAAGTTG 12

RESULT 201
PCT-US02-25943-11543/c
; Sequence 11543, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zsegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 11543
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (1165178)...(1165192)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 12450
PCT-US02-25943-11543

Query Match          57.0%; Score 11.4; DB 1; Length 15;
Score over Length    76.0%;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
Db 14 GTTGACGTTGCCG 2

RESULT 202
US-10-227-565-11543/c
; Sequence 11543, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zsegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 11543
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (1165178)...(1165192)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 12450
US-10-227-565-11543

Query Match          57.0%; Score 11.4; DB 40; Length 15;
Score over Length    76.0%;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
Db 14 GTTGACGTTGCCG 2

RESULT 203
US-10-299-054A-10916

```

```
; Sequence 10916, Application US/10299054A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/299,054A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11910
; SOFTWARE: Proprietary
; SEQ ID NO 10916
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis complete genome.
; FEATURE:
; LOCATION: (3970758)...(3970772)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 13010
US-10-299-054A-10916

Query Match      57.0%; Score 11.4; DB 41; Length 15;
Score over Length 76.0%;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :||||
Db 1 GCCCCAGTTGAAG 13

RESULT 204
US-10-367-832A-11543/C
; Sequence 11543, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 11543
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (1165178)...(1165192)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 12450
US-10-367-832A-11543

Query Match      57.0%; Score 11.4; DB 46; Length 15;
Score over Length 76.0%;
Best Local Similarity 92.3%; Pred. No. 7.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
   ||||| :||||
Db 14 GTTGAAGTTGCCG 2

RESULT 205
US-10-708-953-383591
; Sequence 383591, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 383591
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-708-953-383591

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :||||
Db 3 GCCCCAGTTGAAG 15

RESULT 206
US-10-708-953-409578
; Sequence 409578, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 409578
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-708-953-409578

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :||||
Db 3 GCCCCAGTTGAAG 15

RESULT 207
US-10-708-953-572403
; Sequence 572403, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 572403
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-708-953-572403

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
   ||||| :||||
Db 3 GCCCCAGTTGAAG 15

RESULT 208
US-10-708-953-716806
; Sequence 716806, Application US/10708953
; GENERAL INFORMATION:
```



```
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 716806
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-716806

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 209
US-10-708-953-1012891
; Sequence 1012891, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1012891
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1012891

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 210
US-10-708-953-1276947
; Sequence 1276947, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1276947
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1276947

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 3 GCCCCACUUGAAG 15

; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1931848
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1931848

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 211
US-10-708-953-1931848
; Sequence 1931848, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1931848
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1931848

Query Match      57.0%; Score 11.4; DB 52; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 212
US-10-708-953A-383591
; Sequence 383591, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 383591
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-383591

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAG 13
    ||||| :|||
Db 3 GCCCCACUUGAAG 15

RESULT 213
US-10-708-953A-409578
; Sequence 409578, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
```

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; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 409578
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-409578

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 214
US-10-708-953A-572403
; Sequence 572403, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 572403
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-572403

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 215
US-10-708-953A-716806
; Sequence 716806, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 716806
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-716806

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 216
US-10-708-953A-1012891
; Sequence 1012891, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1012891
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1012891

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 217
US-10-708-953A-1276947
; Sequence 1276947, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1276947
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1276947

Query Match      57.0%; Score 11.4; DB 53; Length 15;
Score over Length 76.0%;
Best Local Similarity 76.9%; Pred. No. 7.9e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAG 13
Db 3 GCCCCACUUGAAG 15

RESULT 218
US-10-708-953A-1931848
; Sequence 1931848, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1931848
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1931848
```

US-10-708-953A-1931848

Query Match 57.0%; Score 11.4; DB 53; Length 15;  
Score over Length 76.0%;  
Best Local Similarity 76.9%; Pred. No. 7.9e+05; Indels 0; Gaps 0;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAAG 13  
| | | | | : | | | |  
Db 3 GCCCAGTTGAAG 15

RESULT 219

US-10-708-952A-102785/c  
; Sequence 102785, Application US/10708952A  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL  
; FILE REFERENCE: 55035  
; CURRENT APPLICATION NUMBER: US/10/708,952A  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 399737  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 102785  
; LENGTH: 13  
; TYPE: RNA  
; ORGANISM: Human adenovirus B (HAdV-B)  
US-10-708-952A-102785

Query Match 49.0%; Score 9.8; DB 51; Length 13;  
Score over Length 75.4%;  
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20  
| | | | | | | | | |  
Db 13 TTGATGTTGCCAT 1

RESULT 220

US-10-708-952A-105521/c  
; Sequence 105521, Application US/10708952A  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL  
; FILE REFERENCE: 55035  
; CURRENT APPLICATION NUMBER: US/10/708,952A  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 399737  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 105521  
; LENGTH: 13  
; TYPE: RNA  
; ORGANISM: Human adenovirus B (HAdV-B)  
US-10-708-952A-105521

Query Match 49.0%; Score 9.8; DB 51; Length 13;  
Score over Length 75.4%;  
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCC 18  
| | | | | | | | | |  
Db 13 AATTGATGTTGCC 1

RESULT 221

US-10-708-952A-281446/c  
; Sequence 281446, Application US/10708952A  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL  
; FILE REFERENCE: 55035  
; CURRENT APPLICATION NUMBER: US/10/708,952A  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 399737  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 281446  
; LENGTH: 13  
; TYPE: RNA  
; ORGANISM: Human adenovirus B (HAdV-B)  
US-10-708-952A-281446

Query Match 49.0%; Score 9.8; DB 51; Length 13;  
Score over Length 75.4%;  
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGCC 18  
| | | | | | | | | |  
Db 13 AATTGATGTTGCC 1

RESULT 222

US-10-708-952A-283324/c  
; Sequence 283324, Application US/10708952A  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL  
; FILE REFERENCE: 55035  
; CURRENT APPLICATION NUMBER: US/10/708,952A  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 399737  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 283324  
; LENGTH: 13  
; TYPE: RNA  
; ORGANISM: Human adenovirus B (HAdV-B)  
US-10-708-952A-283324

Query Match 49.0%; Score 9.8; DB 51; Length 13;  
Score over Length 75.4%;  
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20  
| | | | | | | | | |  
Db 13 TTGATGTTGCCAT 1

RESULT 223

US-10-708-952B-102785/c  
; Sequence 102785, Application US/10708952B  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL  
; FILE REFERENCE: 06087.0301.CPUS00  
; CURRENT APPLICATION NUMBER: US/10/708,952B  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 399738  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 102785  
; LENGTH: 13  
; TYPE: RNA  
; ORGANISM: Human adenovirus B (HAdV-B)  
US-10-708-952B-102785

Query Match 49.0%; Score 9.8; DB 51; Length 13;  
Score over Length 75.4%;  
Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;

```
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCCG 20
DB 13 TTGATGTGCCAT 1

RESULT 224
US-10-708-952B-105521/c
; Sequence 105521, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; NUMBER OF SEQ ID NOS: 2004-04-02
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105521
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HADV-B)
US-10-708-952B-105521
Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGCC 18
DB 13 AATTGATGTGCC 1

RESULT 225
US-10-708-952B-281446/c
; Sequence 281446, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 281446
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HADV-B)
US-10-708-952B-281446
Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AGTTGAAGTTGCC 18
DB 13 AATTGATGTGCC 1

RESULT 226
US-10-708-952B-283324/c
; Sequence 283324, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
```

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; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 283324
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Human adenovirus B (HADV-B)
US-10-708-952B-283324
Query Match 49.0%; Score 9.8; DB 51; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCCG 20
DB 13 TTGATGTGCCAT 1

RESULT 227
US-10-708-953-519962/c
; Sequence 519962, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 519962
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-519962
Query Match 49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCCG 20
DB 13 TTGAAGATGCCAT 1

RESULT 228
US-10-708-953-683001/c
; Sequence 683001, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 683001
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-683001
Query Match 49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTGAAGTTGCCG 20
DB 13 TTGAAGATGCCAT 1
```



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; Sequence 1151132, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1151132
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1151132

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
Db 13 GTTCAGTTGCTG 1

RESULT 235
US-10-708-953-1169509/c
; Sequence 1169509, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1169509
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1169509

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
Db 13 GTTCAGTTGCTG 1

RESULT 236
US-10-708-953-1571840/c
; Sequence 1571840, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1571840
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1571840

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAGT 14
Db 13 CCCAGTGCAGT 1

RESULT 237
US-10-708-953-1618678/c
; Sequence 1618678, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1618678
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1618678

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
Db 13 TTGAAGATGCCAT 1

RESULT 238
US-10-708-953-1873083/c
; Sequence 1873083, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1873083
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1873083

Query Match          49.0%; Score 9.8; DB 52; Length 13;
Score over Length    75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAGT 14
Db 13 CCCAGTGCAGT 1

RESULT 239
US-10-708-953-2013164
; Sequence 2013164, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
```

```
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2013164
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2013164

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 53.8%; Pred. No. 5.1e+06;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
Db 1 UUGAAGGUGUGU 13
      :|||||:|:|:|:
      :|||||:|:|:|:

RESULT 240
US-10-708-953-2083562/c
; Sequence 2083562, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2083562
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2083562

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTCAAGTTGCCG 19
Db 13 GTTCAAGTTGCTG 1
      |||||
      |||||

RESULT 241
US-10-708-953-2156300/c
; Sequence 2156300, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2156300
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2156300

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
Db 13 TTGAAGATGCCAT 1
      |||||
      |||||

RESULT 242
US-10-708-953-2181596/c
; Sequence 2181596, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2181596
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2181596

Query Match      49.0%; Score 9.8; DB 52; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCCAGTTCAAGTT 15
Db 13 CCCAGTTTCAGTT 1
      |||||
      |||||

RESULT 243
US-10-708-953A-519962/c
; Sequence 519962, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519962
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-519962

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
Db 13 TTGAAGATGCCAT 1
      |||||
      |||||

RESULT 244
US-10-708-953A-683001/c
; Sequence 683001, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 683001
; LENGTH: 13
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-683001

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
   ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 245
US-10-708-953A-755878/c
; Sequence 755878, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 755878
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-755878

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
   ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 246
US-10-708-953A-804357/c
; Sequence 804357, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 804357
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-804357

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAGT 14
   ||||| |||||
Db 13 CCCAGTGCAGT 1

RESULT 247
US-10-708-953A-962280/c
; Sequence 962280, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 962280
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-962280

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
   ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 248
US-10-708-953A-1014267
; Sequence 1014267, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1014267
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1014267

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCGT 20
   ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 249
US-10-708-953A-1125006/c
; Sequence 1125006, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1125006
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1125006

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
```



```
; Best Local Similarity 84.6%; Pred. No. 5.1e+06; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2;

QY 8 TTGAAGTTGCCGT 20
    ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 250
US-10-708-953A-1151132/c
; Sequence 1151132, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1151132
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1151132

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTTCAAGTTGCGG 19
    ||||| |||||
Db 13 GTTCAAGTTGCTG 1

RESULT 251
US-10-708-953A-1169509/c
; Sequence 1169509, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1169509
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1169509

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGT 14
    ||||| |||||
Db 13 CCCAGTGCAAGT 1

RESULT 252
US-10-708-953A-1571840/c
; Sequence 1571840, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
```

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; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1571840
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1571840

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTT 15
    ||||| |||||
Db 13 CCCAGTTTCAGTT 1

RESULT 253
US-10-708-953A-1618678/c
; Sequence 1618678, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1618678
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1618678

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCGT 20
    ||||| |||||
Db 13 TTGAAGATGCCAT 1

RESULT 254
US-10-708-953A-1873083/c
; Sequence 1873083, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1873083
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1873083

Query Match 49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGT 14
    ||||| |||||
Db 13 CCCAGTGCAAGT 1
```

```
; ORGANISM: Homo sapiens
US-10-708-953A-2156300

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
Db      13 TTGAAGATGCCAT 1
      ||||| |||||
      ||||| |||||

RESULT 258
US-10-708-953A-2181596/c
; Sequence 2181596, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2181596
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2181596

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CCCAGTTGAAGTT 15
Db      13 CCCAGTTTCAGTT 1
      ||||| |||||
      ||||| |||||

RESULT 259
US-10-709-572-189555/c
; Sequence 189555, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189555
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-189555

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CCCAGTTGAAGT 14
Db      13 CCCCTGCTGAAGT 1
      ||||| |||||
      ||||| |||||

RESULT 260
US-10-709-572-337591/c

; ORGANISM: Homo sapiens
US-10-708-953A-2013164

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 53.8%; Pred. No. 5.1e+06;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCGT 20
Db      1 UUGAAGGUGCUG 13
      :|||: |||:
      :|||: |||:

RESULT 256
US-10-708-953A-2083562/c
; Sequence 2083562, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2083562
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2083562

Query Match      49.0%; Score 9.8; DB 53; Length 13;
Score over Length 75.4%;
Best Local Similarity 84.6%; Pred. No. 5.1e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCCG 19
Db      13 GTTCAAGTTGCTG 1
      ||||| |||||
      ||||| |||||

RESULT 257
US-10-708-953A-2156300/c
; Sequence 2156300, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2156300
; LENGTH: 13
; TYPE: RNA
```

; Sequence 337591, Application US/10709572  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 050992.0202.CPUS01  
; CURRENT APPLICATION NUMBER: US/10709,572  
; CURRENT FILING DATE: 2005-05-14  
; NUMBER OF SEQ ID NOS: 10068324  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 337591  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-709-572-337591

Query Match 49.0%; Score 9.8; DB 53; Length 13;  
Score over Length 75.4%;  
Best Local Similarity 84.6%; Pred. No. 5.1e+06;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCC 18  
|||||  
DB 13 AGTTGAAGAGCC 1

RESULT 261  
PCT-US06-29646A-101428/c  
; Sequence 101428, Application PC/TUS0629646A  
; GENERAL INFORMATION:  
; APPLICANT: GREEN, PAMELA  
; APPLICANT: MEYERS, ELAKE  
; APPLICANT: LU, CHENG  
; APPLICANT: TEJ, SHIVAKUNDAN SINGH  
; APPLICANT: SOURET, FREDERIC  
; TITLE OF INVENTION: SMALL REGULATORY RNAS AND METHODS OF USE  
; FILE REFERENCE: 99689-00009  
; CURRENT APPLICATION NUMBER: PCT/US06/29646A  
; CURRENT FILING DATE: 2006-07-28  
; PRIOR APPLICATION NUMBER: 60/772,666  
; PRIOR FILING DATE: 2006-02-13  
; PRIOR APPLICATION NUMBER: 60/703,215  
; PRIOR FILING DATE: 2005-07-28  
; NUMBER OF SEQ ID NOS: 185413  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 101428  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
PCT-US06-29646A-101428

Query Match 64.0%; Score 12.8; DB 3; Length 17;  
Score over Length 75.3%;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTTGC 17  
|||||  
DB 16 CCCAGGGGAAGTTGC 1

RESULT 262  
US-10-535-164-454911/c  
; Sequence 454911, Application US/10535164  
; GENERAL INFORMATION:  
; APPLICANT: BENTWICH, ITZHAK  
; TITLE OF INVENTION: Bioinformatically detectable of Novel Regulatory genes and thereof  
; FILE REFERENCE: 050992.0200.PCUS13  
; CURRENT APPLICATION NUMBER: US/10/535,164  
; CURRENT FILING DATE: 2005-05-16  
; NUMBER OF SEQ ID NOS: 548156

; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 454911  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Human  
US-10-535-164-454911

Query Match 64.0%; Score 12.8; DB 48; Length 17;  
Score over Length 75.3%;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCC 18  
|||||  
DB 16 CCCAGGTGAAGTTGCC 1

RESULT 263  
US-10-605-923-625220/c  
; Sequence 625220, Application US/10605923  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND  
; FILE REFERENCE: 55000  
; CURRENT APPLICATION NUMBER: US/10/605,923  
; CURRENT FILING DATE: 2003-11-06  
; NUMBER OF SEQ ID NOS: 1515668  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 625220  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-605-923-625220

Query Match 64.0%; Score 12.8; DB 49; Length 17;  
Score over Length 75.3%;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCC 18  
|||||  
DB 16 CCCAGGTGAAGTTGCC 1

RESULT 264  
US-10-707-975B-497939/c  
; Sequence 497939, Application US/10707975B  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Daniel, Kfar  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND  
; FILE REFERENCE: 06087.0201.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/707,975B  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 664008  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 497939  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Human  
US-10-707-975B-497939

Query Match 64.0%; Score 12.8; DB 51; Length 17;  
Score over Length 75.3%;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCC 18  
|||||  
DB 16 CCCAGGTGAAGTTGCC 1

```
RESULT 265
US-11-495-951A-101428/c
; Sequence 101428, Application US/11495951A
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAs AND METHODS OF USE
; FILE REFERENCE: 99689-00009
; CURRENT APPLICATION NUMBER: US/11/495,951A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 101428
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-495-951A-101428

Query Match      64.0%; Score 12.8; DB 77; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAGTTGC 17
   ||||| |||||
Db 16 CCCAGGGGAGTTGC 1

RESULT 266
US-10-708-953-1313224/c
; Sequence 1313224, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1313224
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1313224

Query Match      60.0%; Score 12; DB 52; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3

RESULT 267
US-10-708-953-1811627/c
; Sequence 1811627, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1811627

Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3

RESULT 268
US-10-708-953A-1313224/c
; Sequence 1313224, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1313224
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1313224

Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3

RESULT 269
US-10-708-953A-1811627/c
; Sequence 1811627, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1811627

Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3
```

```
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1811627
```

```
Query Match      60.0%; Score 12; DB 52; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3
```

```
RESULT 268
US-10-708-953A-1313224/c
; Sequence 1313224, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1313224
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1313224
```

```
Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3
```

```
RESULT 269
US-10-708-953A-1811627/c
; Sequence 1811627, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1811627
```

```
Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3
```

```
RESULT 269
US-10-708-953A-1811627/c
; Sequence 1811627, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1811627
```

```
Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3
```

```
RESULT 269
US-10-708-953A-1811627/c
; Sequence 1811627, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1811627
```

```
Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3
```

```
RESULT 269
US-10-708-953A-1811627/c
; Sequence 1811627, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1811627
```

```
Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3
```

```
RESULT 269
US-10-708-953A-1811627/c
; Sequence 1811627, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1811627
```

```
Query Match      60.0%; Score 12; DB 53; Length 16;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
   ||||| |||||
Db 14 CCCAGTTGAAGT 3
```

```
RESULT 269
US-10-708-953A-1811627/c
; Sequence 1811627, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1811627
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1811627
```

```
Db 14 CCCAGTTGAAGT 3

RESULT 270
US-10-257-017B-272526
; Sequence 272526, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 272526
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide-Primer
US-10-257-017B-272526

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 4 AGTTGAAGT 12

RESULT 271
US-10-257-017B-281370/c
; Sequence 281370, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281370
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009690
US-10-257-017B-281370

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15
Db 11 GTTGAAGTT 3

RESULT 272
US-10-257-017B-284630/c
; Sequence 284630, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

```
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 284630
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011911
US-10-257-017B-284630

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 12 AGTTGAAGT 4

RESULT 273
US-10-257-017B-288152
; Sequence 288152, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 288152
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013396
US-10-257-017B-288152

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 2 TTGAAGTTG 10

RESULT 274
US-10-257-017B-298602
; Sequence 298602, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 298602  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018187  
US-10-257-017B-298602

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGAAGTTGC 17  
Db 4 TGAAGTTGC 12  
|||||

RESULT 275  
US-10-257-017B-298745  
; Sequence 298745, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 298745  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonukleotid-Primer  
US-10-257-017B-298745

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15  
Db 4 GTTGAAGTT 12  
|||||

RESULT 276  
US-10-257-017B-299931  
; Sequence 299931, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 299931  
; LENGTH: 12  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018813  
US-10-257-017B-299931

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16  
Db 2 TTGAAGTTG 10  
|||||

RESULT 277  
US-10-257-017B-303341/c  
; Sequence 303341, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 303341  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020445  
US-10-257-017B-303341

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14  
Db 11 AGTTGAAGT 3  
|||||

RESULT 278  
US-10-257-017B-305026  
; Sequence 305026, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 305026  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021217  
US-10-257-017B-305026

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;

```
Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 7 GTTGAAGTT 15
Db 4 GTTGAAGTT 12

RESULT 279
US-10-257-017B-307994
; Sequence 307994, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307994
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022828
US-10-257-017B-307994

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 7 GTTGAAGTT 15
Db 4 GTTGAAGTT 12

RESULT 280
US-10-257-017B-310012
; Sequence 310012, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310012
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023776
US-10-257-017B-310012

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 8 TTGAAGTTG 16
Db 2 TTGAAGTTG 10
```

```
RESULT 281
US-10-257-017B-319646/c
; Sequence 319646, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 319646
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029341
US-10-257-017B-319646

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 8 TTGAAGTTG 16
Db 12 TTGAAGTTG 4

RESULT 282
US-10-257-017B-332564/c
; Sequence 332564, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 332564
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036994
US-10-257-017B-332564

Query Match 45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 8 TTGAAGTTG 16
Db 12 TTGAAGTTG 4

RESULT 283
US-10-257-017B-333972
; Sequence 333972, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 333972
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037861
US-10-257-017B-333972

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TTGAAGTTG 16
      |||||
Db      2 TTGAAGTTG 10

RESULT 284
US-10-257-017B-337673
; Sequence 337673, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337673
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039994
US-10-257-017B-337673

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TTGAAGTTG 16
      |||||
Db      2 TTGAAGTTG 10

RESULT 285
US-10-257-017B-338530/c
; Sequence 338530, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338530
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005251
US-10-257-017B-338530

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TTGAAGTTG 16
      |||||
Db      12 TTGAAGTTG 4

RESULT 286
US-10-257-017B-338626/c
; Sequence 338626, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338626
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040587
US-10-257-017B-338626

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GTTGAAGTT 15
      |||||
Db      9 GTTGAAGTT 1

RESULT 287
US-10-257-017B-342781
; Sequence 342781, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 342781
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```



; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042707  
US-10-257-017B-342781

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16  
| | | | | | | |  
DB 1 TTGAAGTTG 9

RESULT 288  
US-10-257-017B-343923/c  
; Sequence 343923, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 343923  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043299  
US-10-257-017B-343923

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15  
| | | | | | | |  
DB 10 GTTGAAGTT 2

RESULT 289  
US-10-257-017B-345821/c  
; Sequence 345821, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 345821  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044228  
US-10-257-017B-345821

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15  
| | | | | | | |  
DB 9 GTTGAAGTT 1

RESULT 290  
US-10-257-017B-358109  
; Sequence 358109, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 358109  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050957  
US-10-257-017B-358109

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16  
| | | | | | | |  
DB 1 TTGAAGTTG 9

RESULT 291  
US-10-257-017B-360215/c  
; Sequence 360215, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 360215  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051979  
US-10-257-017B-360215

Query Match 45.0%; Score 9; DB 40; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14  
| | | | | | | |  
DB 10 AGTTGAAGT 2

RESULT 292

```
US-10-257-017B-365894/c
; Sequence 365894, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 365894
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0055428
US-10-257-017B-365894

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TTGAAGTTG 16
Db      12 TTGAAGTTG 4

RESULT 293
US-10-257-017B-369254
; Sequence 369254, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369254
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057554
US-10-257-017B-369254

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GTTGAAGTT 15
Db      4 GTTGAAGTT 12

RESULT 294
US-10-257-017B-369635/c
; Sequence 369635, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

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US-10-257-017B-369635
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369635
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057764
US-10-257-017B-369635

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TTGAAGTTG 16
Db      9 TTGAAGTTG 1

RESULT 295
US-10-257-017B-379943
; Sequence 379943, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379943
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063547
US-10-257-017B-379943

Query Match      45.0%; Score 9; DB 40; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 AGTTGAAGT 14
Db      4 AGTTGAAGT 12

RESULT 296
US-10-708-953-1574359/c
; Sequence 1574359, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1574359
; LENGTH: 12
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
US-10-708-953-1574359

Query Match      45.0%; Score 9; DB 52; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 297
US-10-708-953-1983714/c
; Sequence 1983714, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1983714
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1983714

Query Match      45.0%; Score 9; DB 52; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 298
US-10-708-953-2023470/c
; Sequence 2023470, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2023470
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2023470

Query Match      45.0%; Score 9; DB 52; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 299
US-10-708-953-2107113/c
; Sequence 2107113, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2107113
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2107113

Query Match      45.0%; Score 9; DB 52; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 300
US-10-708-953A-1574359/c
; Sequence 1574359, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1574359
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1574359

Query Match      45.0%; Score 9; DB 53; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 301
US-10-708-953A-1983714/c
; Sequence 1983714, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1983714
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1983714

Query Match      45.0%; Score 9; DB 53; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4

RESULT 302
US-10-708-953A-1983714/c
; Sequence 1983714, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1983714
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1983714

Query Match      45.0%; Score 9; DB 53; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 11
   |||||
Db 12 CCCAGTTGAA 4
```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAGTTGA 11  
|||  
Db 12 CCAGTTGA 4

## RESULT 302

US-10-708-953A-2023470/c  
; Sequence 2023470, Application US/10708953A  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953A  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2023470  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953A-2023470

Query Match 45.0%; Score 9; DB 53; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAA 12  
|||  
Db 11 CCAGTTGAA 3

## RESULT 303

US-10-708-953A-2107113/c  
; Sequence 2107113, Application US/10708953A  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953A  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2107113  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953A-2107113

Query Match 45.0%; Score 9; DB 53; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAA 12  
|||  
Db 10 CCAGTTGAA 2

## RESULT 304

US-09-168-519A-14/c  
; Sequence 14, Application US/09168519A  
; GENERAL INFORMATION:  
; APPLICANT: Richelson, Elliott  
; APPLICANT: Jansen, Karen  
; TITLE OF INVENTION: Using Polyamide Nucleic Acid Oligomers  
; FILE REFERENCE: 07039-107001  
; CURRENT APPLICATION NUMBER: US/09/168,519A

; CURRENT FILING DATE: 1998-10-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-168-519A-14

Query Match 52.0%; Score 10.4; DB 20; Length 14;  
Score over Length 74.3%;  
Best Local Similarity 91.7%; Pred. No. 2.5e+06;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16  
|||  
Db 14 CAGATGAAGTTG 3

## RESULT 305

US-10-708-953-635436  
; Sequence 635436, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 635436  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-635436

Query Match 52.0%; Score 10.4; DB 52; Length 14;  
Score over Length 74.3%;  
Best Local Similarity 75.0%; Pred. No. 2.5e+06;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAA 12  
|||  
Db 3 GCUCCAGUUGAA 14

## RESULT 306

US-10-708-953-842460  
; Sequence 842460, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 842460  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-842460

Query Match 52.0%; Score 10.4; DB 52; Length 14;  
Score over Length 74.3%;  
Best Local Similarity 75.0%; Pred. No. 2.5e+06;  
Matches .9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAA 12

```
Db      3  GCUCCAGUUGAA 14
|||:|:|:|
RESULT 307
US-10-708-953-1763210
; Sequence 1763210, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1763210
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1763210
Query Match      52.0%; Score 10.4; DB 52; Length 14;
Score over Length 74.3%;
Best Local Similarity 75.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAA 12
|||:|:|:|
Db      3  GCUCCAGUUGAA 14
|||:|:|:|
RESULT 310
US-10-708-953A-1763210
; Sequence 1763210, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1763210
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1763210
Query Match      52.0%; Score 10.4; DB 53; Length 14;
Score over Length 74.3%;
Best Local Similarity 75.0%; Pred. No. 2.5e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAA 12
|||:|:|:|
Db      3  GCUCCAGUUGAA 14
|||:|:|:|
RESULT 311
US-10-709-572-147851/c
; Sequence 147851, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 147851
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-147851
Query Match      52.0%; Score 10.4; DB 53; Length 14;
Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5  CAGTTGAAGTTG 16
|||:|:|:|
Db     14  CACTTGAAGTTG 3
|||:|:|:|
```

```
RESULT 312
US-10-799-238-14/c
; SEQUENCE 14, Application US/10799238
; GENERAL INFORMATION:
; APPLICANT: Richelson, Elliott
; APPLICANT: Tyler, Beth Marie
; APPLICANT: Cusack, Bernadette Marie
; APPLICANT: Douglas, Christopher Lee
; APPLICANT: Jansen, Karen
; TITLE OF INVENTION: USING POLYAMIDE NUCLEIC ACID OLIGOMERS
; TITLE OF INVENTION: TO ENGENDER A BIOLOGICAL RESPONSE
; FILE REFERENCE: 07039/126001
; CURRENT APPLICATION NUMBER: US/10799,238
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US/09/168,791
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Rat
US-10-799-238-14
Query Match      52.0%; Score 10.4; DB 57; Length 14;
Score over Length 74.3%;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
DB 14 CAGATGAAGTTG 3

RESULT 313
US-10-257-017B-61663
; SEQUENCE 61663, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 61663
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016401
US-10-257-017B-61663
Query Match      48.0%; Score 9.6; DB 40; Length 13;
Score over Length 73.8%;
Best Local Similarity 90.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTGC 17
DB 4 TTGAAGTTGY 13

RESULT 314
US-10-257-017B-61664/c
; SEQUENCE 61664, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 61664
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016401
US-10-257-017B-61664
Query Match      48.0%; Score 9.6; DB 40; Length 13;
Score over Length 73.8%;
Best Local Similarity 90.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTGC 17
DB 10 TTGAAGTTGY 1

RESULT 315
PCT-US02-25943-533
; SEQUENCE 533, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 533
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (50175)...(50190)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 574
PCT-US02-25943-533
Query Match      59.0%; Score 11.8; DB 1; Length 16;
Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGC 17
DB 1 CCCAGTTGCAGGTGC 15

RESULT 316
US-09-708-690-5807
; SEQUENCE 5807, Application US/09708690
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00,876-L (400/002)
; CURRENT APPLICATION NUMBER: US/09/708,690
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
```

; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/685,664  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 20828  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5807  
; LENGTH: 16  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-708-690-5807

Query Match 59.0%; Score 11.8; DB 30; Length 16;  
Score over Length 73.8%;  
Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 2;

Qy 1 GCCCCAGTTGAAGTT 15  
| | | | | : | | | | :  
Db 2 GACCCAGAUGAAGUU 16

## RESULT 317

US-09-870-161-5807  
; Sequence 5807, Application US/09870161  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-M (400/026)  
; CURRENT APPLICATION NUMBER: US/09/870,161  
; CURRENT FILING DATE: 2001-08-27  
; NUMBER OF SEQ ID NOS: 20821  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5807  
; LENGTH: 16  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-870-161-5807

Query Match 59.0%; Score 11.8; DB 33; Length 16;  
Score over Length 73.8%;  
Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 2;

Qy 1 GCCCCAGTTGAAGTT 15  
| | | | | : | | | | :  
Db 2 GACCCAGAUGAAGUU 16

## RESULT 318

US-10-227-565-533  
; Sequence 533, Application US/10227565  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/227,565  
; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 64158  
; SOFTWARE: Proprietary  
; SEQ ID NO 533  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
; FEATURE:  
; LOCATION: (50175)...(50190)

; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 574  
US-10-227-565-533

Query Match 59.0%; Score 11.8; DB 40; Length 16;  
Score over Length 73.8%;  
Best Local Similarity 86.7%; Pred. No. 5e+05; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 2;

Qy 3 CCCAGTTGAAGTTGC 17  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 CCCAGTTGCAGGTGC 15

## RESULT 319

US-10-287-949A-5807  
; Sequence 5807, Application US/10287949A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5807  
; LENGTH: 16  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-5807

Query Match 59.0%; Score 11.8; DB 41; Length 16;  
Score over Length 73.8%;  
Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 2;

Qy 1 GCCCCAGTTGAAGTT 15  
| | | | | : | | | | :  
Db 2 GACCCAGAUGAAGUU 16

## RESULT 320

US-10-287-949B-5807  
; Sequence 5807, Application US/10287949B  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: 00-876-O (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949B  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 20824  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5807  
; LENGTH: 16  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949B-5807

Query Match 59.0%; Score 11.8; DB 41; Length 16;  
Score over Length 73.8%;  
Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 2;

Qy 1 GCCCCAGTTGAAGTT 15

```
Db      2  GACCCAGGAUGAUU 16
      | ||||| :|||::
      | ||||| :|||::

RESULT 321
US-10-287-949C-5807
; Sequence 5807, Application US/10287949C
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: 00-876-O (400/053)
; CURRENT APPLICATION NUMBER: US/10/287,949C
; NUMBER OF SEQ ID NOS: 20824
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949C-5807

Query Match      59.0%; Score 11.8; DB 41; Length 16;
Score over Length 73.8%;
Best Local Similarity 66.7%; Pred. No. 5e+05;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1  GCCCCAGTTGAAGTTT 15
      | ||||| :|||::
      | ||||| :|||::
Db      2  GACCCAGGAUGAUU 16

RESULT 322
US-10-367-832A-533
; Sequence 533, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 533
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (50175)...(50190)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 574
US-10-367-832A-533

Query Match      59.0%; Score 11.8; DB 46; Length 16;
Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3  CCAAGTTGAAGTTGC 17
      | ||||| :|||::
      | ||||| :|||::
Db      1  CCAAGTTGAAGTTGC 15

RESULT 323
US-10-709-572-191130/c
; Sequence 191130, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
```

```
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191130
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-191130

Query Match      59.0%; Score 11.8; DB 53; Length 16;
Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2  CCCCAGTTGAAGTTG 16
      | ||||| :|||::
      | ||||| :|||::
Db      16  CCCCCTGCTGAAGTTG 2

RESULT 324
US-10-709-572-191264/c
; Sequence 191264, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191264
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-191264

Query Match      59.0%; Score 11.8; DB 53; Length 16;
Score over Length 73.8%;
Best Local Similarity 86.7%; Pred. No. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2  CCCCAGTTGAAGTTG 16
      | ||||| :|||::
      | ||||| :|||::
Db      15  CCCCCTGCTGAAGTTG 1

RESULT 325
US-11-088-219-5807
; Sequence 5807, Application US/11088219
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; FILE REFERENCE: MEHB00-876-O (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
```



; PRIOR APPLICATION NUMBER: 09/371,722  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 08/584,040  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5807  
; LENGTH: 16  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-088-219A-5807

Query Match 59.0%; Score 11.8; DB 63; Length 16;  
Score over Length 73.8%;  
Best Local Similarity 66.7%; Pred. No. 5e+05; 2; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 3;

QY 1 GCCCCAGTTGAAGTT 15  
| | | | | : | | | | |  
Db 2 GACCCAGAUGAAGUU 16

RESULT 326  
US-11-088-219A-5807  
; Sequence 5807, Application US/11088219A  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or  
; TITLE OF INVENTION: Conditions  
; TITLE OF INVENTION: Related to Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: 400/266 (MBH00-876-Q)  
; CURRENT APPLICATION NUMBER: US/11/088,219A  
; CURRENT FILING DATE: 2005-03-23  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5807  
; LENGTH: 16  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-088-219A-5807

Query Match 59.0%; Score 11.8; DB 63; Length 16;  
Score over Length 73.8%;  
Best Local Similarity 66.7%; Pred. No. 5e+05; 2; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 3;

QY 1 GCCCCAGTTGAAGTT 15  
| | | | | : | | | | |  
Db 2 GACCCAGAUGAAGUU 16

RESULT 327  
PCT-US03-36787-764639/c  
; Sequence 764639, Application PC/TUS0336787  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Read, Steven  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Methods and Compositions for Improving  
; TITLE OF INVENTION: siRNA functionality  
; FILE REFERENCE: 13499PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/36787  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
PCT-US03-36787-764639

Query Match 70.0%; Score 14; DB 2; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20  
| | | | | : | | | | |  
Db 16 GTTGAAGTTGCCGT 3

RESULT 328  
US-10-714-333A-764639/c  
; Sequence 764639, Application US/10714333A  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333A  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-714-333A-764639

Query Match 70.0%; Score 14; DB 54; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20  
| | | | | : | | | | |  
Db 16 GTTGAAGTTGCCGT 3

RESULT 329  
US-10-714-333B-764639/c  
; Sequence 764639, Application US/10714333B  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333B  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-714-333B-764639

Query Match 70.0%; Score 14; DB 55; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCGT 20  
|||||  
Db 16 GTTGAAGTTGCCGT 3

## RESULT 330

US-10-714-333C-764639/c  
; Sequence 764639, Application US/10714333C  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333C  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-714-333C-764639

Query Match 70.0%; Score 14; DB 56; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCGT 20  
|||||  
Db 16 GTTGAAGTTGCCGT 3

## RESULT 331

US-11-083-784-764639/c  
; Sequence 764639, Application US/11083784  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-764639

Query Match 70.0%; Score 14; DB 63; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCGT 20  
|||||  
Db 16 GTTGAAGTTGCCGT 3

## RESULT 332

US-11-093-832-764639/c  
; Sequence 764639, Application US/11093832  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/093,832  
; CURRENT FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-093-832-764639

Query Match 70.0%; Score 14; DB 64; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCGT 20  
|||||  
Db 16 GTTGAAGTTGCCGT 3

## RESULT 333

US-11-095-383-764639/c  
; Sequence 764639, Application US/11095383  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/095,383  
; CURRENT FILING DATE: 2005-03-30

; PRIOR APPLICATION NUMBER: 10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-095-383-764639

Query Match 70.0%; Score 14; DB 65; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GTTGAAGTTGCCGT 20  
|||||  
Db 16 GTTGAAGTTGCCGT 3

RESULT 334  
US-11-101-244-764639/c  
; Sequence 764639, Application US/1101244  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-764639

Query Match 70.0%; Score 14; DB 66; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GTTGAAGTTGCCGT 20  
|||||  
Db 16 GTTGAAGTTGCCGT 3

RESULT 335  
US-11-313-452-764639/c  
; Sequence 764639, Application US/11313452  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/313,452

; CURRENT FILING DATE: 2005-12-21  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-313-452-764639

Query Match 70.0%; Score 14; DB 71; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GTTGAAGTTGCCGT 20  
|||||  
Db 16 GTTGAAGTTGCCGT 3

RESULT 336  
US-11-313-452A-764639/c  
; Sequence 764639, Application US/11313452A  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/313,452A  
; CURRENT FILING DATE: 2005-12-21  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-313-452A-764639

Query Match 70.0%; Score 14; DB 72; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GTTGAAGTTGCCGT 20  
|||||  
Db 16 GTTGAAGTTGCCGT 3

RESULT 337  
US-10-299-054A-4597  
; Sequence 4597, Application US/10299054A  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/299,054A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 11910  
; SOFTWARE: Proprietary  
; SEQ ID NO 4597  
; LENGTH: 18  
; TYPE: DNA

```
; ORGANISM: Mycobacterium tuberculosis complete genome.
; FEATURE:
; LOCATION: (1751704)...(1751721)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 5545
US-10-299-054A-4597

Query Match      66.0%; Score 13.2; DB 41; Length 18;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 9.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTTGCCG 19
   ||| ||||| ||||| |||||
Db 1 CCCAGTTGAAGAGCCG 18

RESULT 338
US-09-274-553-2617/c
; Sequence 2617, Application US/09274553A
; GENERAL INFORMATION:
; APPLICANT: RIBOZYME PHARMACEUTICALS, INC.
; APPLICANT: 2950 Wilderness Place
; APPLICANT: Boulder, Colorado 80301
; APPLICANT: USA
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS RELATED TO HEPATITIS C
; TITLE OF INVENTION: VIRUS INFECTION
; FILE REFERENCE: 241/078-PCT
; CURRENT APPLICATION NUMBER: US/09/274,553A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3118
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2617
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-274-553-2617

Query Match      55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
   ||| ||||| |||||
Db 15 CCCAGTTGAAG 5

RESULT 339
US-09-274-553B-1284/c
; Sequence 1284, Application US/09274553B
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: tpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553B
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
```

```
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553B-1284

Query Match      55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
   ||| ||||| |||||
Db 15 CCCAGTTGAAG 5

RESULT 340
US-09-274-553C-1284/c
; Sequence 1284, Application US/09274553C
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: tpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553C
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553C-1284

Query Match      55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13
   ||| ||||| |||||
Db 15 CCCAGTTGAAG 5

RESULT 341
US-09-274-553D-1284/c
; Sequence 1284, Application US/09274553D
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
```

```
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1284

Query Match 55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 342
US-09-274-553E-1284/c
; Sequence 1284, Application US/09274553E
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553E
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553E-1284

Query Match 55.0%; Score 11; DB 21; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 343
US-09-274-553B-1284/c
; Sequence 1284, Application US/09504231B
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09504231B
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3258
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231B-1284

Query Match 55.0%; Score 11; DB 24; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13
Db 15 CCCAGTTGAAG 5

RESULT 344
US-09-504-231B-1284/c
; Sequence 1284, Application US/09504231B
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: MBHB00-801-A (247/282)
; CURRENT APPLICATION NUMBER: US/09/504,231B
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3258
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1284
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231B-1284

Query Match 55.0%; Score 11; DB 24; Length 15;
Score over Length 73.3%;
```

Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13  
Db 15 CCCAGTTGAAG 5

RESULT 345  
US-09-611-931A-1284/c  
; Sequence 1284, Application US/09611931  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: FDI 250/285  
; CURRENT APPLICATION NUMBER: US/09/611,931  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1284  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-611-931-1284

Query Match 55.0%; Score 11; DB 27; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13  
Db 15 CCCAGTTGAAG 5

RESULT 346  
US-09-611-931A-1284/c  
; Sequence 1284, Application US/09611931A  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: MEHB00-801-B (250/285)  
; CURRENT APPLICATION NUMBER: US/09/611,931A  
; CURRENT FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242

Query Match 55.0%; Score 11; DB 27; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAG 13  
Db 15 CCCAGTTGAAG 5

RESULT 347  
US-09-708-690-4150/c  
; Sequence 4150, Application US/09708690  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor  
; FILE REFERENCE: MEHB00,876-L (400/002)  
; CURRENT APPLICATION NUMBER: US/09/708,690  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/685,664  
; PRIOR FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 20828  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-708-690-4150

Query Match 55.0%; Score 11; DB 30; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
Db 15 CCAGTTGAAGT 5

RESULT 348  
US-09-870-161-4150/c  
; Sequence 4150, Application US/09870161  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor  
; FILE REFERENCE: MEHB00-876-M (400/026)  
; CURRENT APPLICATION NUMBER: US/09/870,161  
; CURRENT FILING DATE: 2001-08-27  
; NUMBER OF SEQ ID NOS: 20821  
; SOFTWARE: PatentIn version 3.0

Query Match 55.0%; Score 11; DB 30; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
Db 15 CCAGTTGAAGT 5

RESULT 349  
US-09-870-161-4150/c  
; Sequence 4150, Application US/09870161  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor  
; FILE REFERENCE: MEHB00-876-M (400/026)  
; CURRENT APPLICATION NUMBER: US/09/870,161  
; CURRENT FILING DATE: 2001-08-27  
; NUMBER OF SEQ ID NOS: 20821  
; SOFTWARE: PatentIn version 3.0

Query Match 55.0%; Score 11; DB 30; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
Db 15 CCAGTTGAAGT 5

RESULT 350  
US-09-870-161-4150/c  
; Sequence 4150, Application US/09870161  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor  
; FILE REFERENCE: MEHB00-876-M (400/026)  
; CURRENT APPLICATION NUMBER: US/09/870,161  
; CURRENT FILING DATE: 2001-08-27  
; NUMBER OF SEQ ID NOS: 20821  
; SOFTWARE: PatentIn version 3.0

Query Match 55.0%; Score 11; DB 30; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGT 14  
Db 15 CCAGTTGAAGT 5

; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-870-161-4150

Query Match 55.0%; Score 11; DB 33; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
| | | | | | | | | |  
Db 15 CCAGTTGAAGT 5

## RESULT 349

US-10-287-949A-4150/c  
; Sequence 4150, Application US/10287949A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-4150

Query Match 55.0%; Score 11; DB 41; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
| | | | | | | | | |  
Db 15 CCAGTTGAAGT 5

## RESULT 350

US-10-287-949B-4150/c  
; Sequence 4150, Application US/10287949B  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00-876-O (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949B  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 20824  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949B-4150

Query Match 55.0%; Score 11; DB 41; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-870-161-4150

Query Match 55.0%; Score 11; DB 33; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
| | | | | | | | | |  
Db 15 CCAGTTGAAGT 5

## RESULT 351

US-10-287-949C-4150/c  
; Sequence 4150, Application US/10287949C  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00-876-O (400/053)  
; CURRENT APPLICATION NUMBER: US/10/287,949C  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 20824  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949C-4150

Query Match 55.0%; Score 11; DB 41; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
| | | | | | | | | |  
Db 15 CCAGTTGAAGT 5

## RESULT 352

US-10-951-303-4150/c  
; Sequence 4150, Application US/10951303  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/10/951,303  
; CURRENT FILING DATE: 2004-09-27  
; PRIOR APPLICATION NUMBER: US/09/685,664  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-951-303-4150

Query Match 55.0%; Score 11; DB 60; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-870-161-4150

Query Match 55.0%; Score 11; DB 33; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
| | | | | | | | | |  
Db 15 CCAGTTGAAGT 5

## RESULT 353

US-10-287-949D-4150/c  
; Sequence 4150, Application US/10287949D  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949D  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949D-4150

Query Match 55.0%; Score 11; DB 41; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
| | | | | | | | | |  
Db 15 CCAGTTGAAGT 5

## RESULT 354

US-10-287-949E-4150/c  
; Sequence 4150, Application US/10287949E  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00-876-O (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949E  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 20824  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949E-4150

Query Match 55.0%; Score 11; DB 41; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      4 CCAGTTGAAGT 14
Db      15 CCAGTTGAAGT 5

RESULT 353
US-10-951-303B-4150/c
; Sequence 4150, Application US/10951303B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions
; FILE REFERENCE: 400/158 (MBH00-876-P)
; CURRENT APPLICATION NUMBER: US/10/951.303B
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8228
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-951-303B-4150

Query Match      55.0%; Score 11; DB 60; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CCAGTTGAAGT 14
Db      15 CCAGTTGAAGT 5

RESULT 354
US-11-088-219-4150/c
; Sequence 4150, Application US/11088219
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor
; FILE REFERENCE: MBH00-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
```

```
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-4150

Query Match      55.0%; Score 11; DB 63; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CCAGTTGAAGT 14
Db      15 CCAGTTGAAGT 5

RESULT 355
US-11-088-219A-4150/c
; Sequence 4150, Application US/11088219A
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor
; FILE REFERENCE: 400/266 (MBH00-876-Q)
; CURRENT APPLICATION NUMBER: US/11/088,219A
; CURRENT FILING DATE: 2005-03-23
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4150
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219A-4150

Query Match      55.0%; Score 11; DB 63; Length 15;
Score over Length 73.3%;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CCAGTTGAAGT 14
Db      15 CCAGTTGAAGT 5

RESULT 356
PCT-IL05-00263-27/c
; Sequence 27, Application PC/TIL0500263
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 29323
; CURRENT APPLICATION NUMBER: PCT/IL05/00263
; CURRENT FILING DATE: 2005-03-06
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
PCT-IL05-00263-27

Query Match      44.0%; Score 8.8; DB 1; Length 12;
Score over Length 73.3%;
```



```
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16
   ||| ||| ||| |||
Db 12 CAGCTGAAGTTG 1

RESULT 357
PCT-IL05-00263-29/c
; Sequence 29, Application PC/TIL0500263
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 29323
; CURRENT APPLICATION NUMBER: PCT/IL05/00263
; CURRENT FILING DATE: 2005-03-06
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
PCT-IL05-00263-29

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16
   ||| ||| ||| |||
Db 12 CAGCTGAAGCTG 1

RESULT 358
PCT-IL05-00263-45/c
; Sequence 45, Application PC/TIL0500263
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 29323
; CURRENT APPLICATION NUMBER: PCT/IL05/00263
; CURRENT FILING DATE: 2005-03-06
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
PCT-IL05-00263-45

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16
   ||| ||| ||| |||
Db 12 CAGTTGAACCTG 1

RESULT 359
PCT-US02-15103A-15
; Sequence 15, Application PC/TUS0215103A
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF MARYLAND, BALTIMORE
```

```
; APPLICANT: GONG, Da-Wei
; APPLICANT: SCHULDINER, Alan
; APPLICANT: YANG, Rongze
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE
; FILE REFERENCE: DG-2001-032
; CURRENT APPLICATION NUMBER: PCT/US02/15103A
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/290,829
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 3'clip
; LOCATION: (1)...(12)
; OTHER INFORMATION: ALT2 Exon 3, intron/exon junction, 3' splice acceptor
PCT-US02-15103A-15

Query Match 44.0%; Score 8.8; DB 1; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
   ||| ||| ||| |||
Db 1 CCCAGGTGATG 12

RESULT 360
PCT-US07-68401-1512
; Sequence 1512, Application PC/TUS0768401
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Richard S. Geary
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Punit P. Seth
; APPLICANT: Andrew M. Siwkowski
; APPLICANT: Eric E. Swayze
; APPLICANT: Edward Wanczewitz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: CORE0061US7
; CURRENT APPLICATION NUMBER: PCT/US07/68401
; CURRENT FILING DATE: 2007-05-25
; PRIOR APPLICATION NUMBER: PCT/US2007/061183
; PRIOR FILING DATE: 2007-01-27
; PRIOR APPLICATION NUMBER: 60/746,631
; PRIOR FILING DATE: 2006-05-05
; PRIOR APPLICATION NUMBER: 60/747,059
; PRIOR FILING DATE: 2006-05-11
; PRIOR APPLICATION NUMBER: 60/805,660
; PRIOR FILING DATE: 2006-06-23
; PRIOR APPLICATION NUMBER: 60/864,554
; PRIOR FILING DATE: 2006-11-06
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1512
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
PCT-US07-68401-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 6 AGTTGAAGTTGC 17  
|||||||  
Db 1 AGTTGAAATTC 12

RESULT 361  
PCT-US07-68402-1512  
; Sequence 1512, Application PC/TUS0768402  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wancewitz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: EXPRESSION OF PTP1B  
; FILE REFERENCE: CORE0061W015  
; CURRENT APPLICATION NUMBER: PCT/US07/68402  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1512  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68402-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17  
|||||||  
Db 1 AGTTGAAATTC 12

RESULT 362  
PCT-US07-68403-1512  
; Sequence 1512, Application PC/TUS0768403  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wancewitz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: EXPRESSION OF APOB  
; FILE REFERENCE: CORE0061W08  
; CURRENT APPLICATION NUMBER: PCT/US07/68403  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183

; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1512  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68403-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17  
|||||||  
Db 1 AGTTGAAATTC 12

RESULT 363  
PCT-US07-68404-1512  
; Sequence 1512, Application PC/TUS0768404  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wancewitz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: EXPRESSION OF PCSK9  
; FILE REFERENCE: CORE0061W010  
; CURRENT APPLICATION NUMBER: PCT/US07/68404  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1512  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68404-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17

Db 1 AGTTGAAATTC 12

## RESULT 364

PCT-US07-68406-1512

Sequence 1512, Application PC/TUS0768406

GENERAL INFORMATION:

APPLICANT: Isis Pharmaceuticals, Inc.

APPLICANT: Sanjay Bhanot

APPLICANT: Richard S. Geary

APPLICANT: Robert McKay

APPLICANT: Brett P. Monia

APPLICANT: Punit P. Seth

APPLICANT: Andrew M. Siwkowski

APPLICANT: Eric E. Swayze

APPLICANT: Edward Wancewitz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

FILE REFERENCE: EXPRESSION OF SGLT2

CURRENT FILING DATE: 2007-05-25

PRIOR APPLICATION NUMBER: PCT/US07/68406

PRIOR FILING DATE: 2007-01-27

PRIOR APPLICATION NUMBER: 60/746,631

PRIOR FILING DATE: 2006-05-05

PRIOR APPLICATION NUMBER: 60/747,059

PRIOR FILING DATE: 2006-05-11

PRIOR APPLICATION NUMBER: 60/805,660

PRIOR FILING DATE: 2006-06-23

PRIOR APPLICATION NUMBER: 60/864,554

PRIOR FILING DATE: 2006-11-06

NUMBER OF SEQ ID NOS: 1576

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1512

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

PCT-US07-68406-1512

Query Match

Score over Length 44.0%; Score 8.8; DB 3; Length 12;

Best Local Similarity 73.3%; Pred. No. 1.6e+07;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17

1 AGTTGAAATTC 12

## RESULT 365

PCT-US07-68408-1512

Sequence 1512, Application PC/TUS0768408

GENERAL INFORMATION:

APPLICANT: Isis Pharmaceuticals, Inc.

APPLICANT: Sanjay Bhanot

APPLICANT: Richard S. Geary

APPLICANT: Robert McKay

APPLICANT: Brett P. Monia

APPLICANT: Punit P. Seth

APPLICANT: Andrew M. Siwkowski

APPLICANT: Eric E. Swayze

APPLICANT: Edward Wancewitz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

FILE REFERENCE: EXPRESSION OF CRP

CURRENT FILING DATE: 2007-05-25

PRIOR APPLICATION NUMBER: PCT/US07/68408

PRIOR FILING DATE: 2007-01-27

PRIOR APPLICATION NUMBER: 60/746,631

PRIOR FILING DATE: 2006-05-11

PRIOR APPLICATION NUMBER: 60/805,660

PRIOR FILING DATE: 2006-06-23

PRIOR APPLICATION NUMBER: 60/864,554

PRIOR FILING DATE: 2006-11-06

NUMBER OF SEQ ID NOS: 1576

SOFTWARE: FastSeq for Windows Version 4.0

PRIOR FILING DATE: 2006-05-05  
PRIOR APPLICATION NUMBER: 60/747,059  
PRIOR FILING DATE: 2006-05-11  
PRIOR APPLICATION NUMBER: 60/805,660  
PRIOR FILING DATE: 2006-06-23  
PRIOR APPLICATION NUMBER: 60/864,554  
PRIOR FILING DATE: 2006-11-06  
NUMBER OF SEQ ID NOS: 1576  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1512  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68408-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17

1 AGTTGAAATTC 12

## RESULT 366

PCT-US07-68410-1512

Sequence 1512, Application PC/TUS0768410

GENERAL INFORMATION:

APPLICANT: Isis Pharmaceuticals, Inc.

APPLICANT: Sanjay Bhanot

APPLICANT: Richard S. Geary

APPLICANT: Robert McKay

APPLICANT: Brett P. Monia

APPLICANT: Punit P. Seth

APPLICANT: Andrew M. Siwkowski

APPLICANT: Eric E. Swayze

APPLICANT: Edward Wancewitz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

FILE REFERENCE: EXPRESSION OF GCCR

CURRENT FILING DATE: 2007-05-25

PRIOR APPLICATION NUMBER: PCT/US07/68410

PRIOR FILING DATE: 2007-01-27

PRIOR APPLICATION NUMBER: 60/746,631

PRIOR FILING DATE: 2006-05-05

PRIOR APPLICATION NUMBER: 60/747,059

PRIOR FILING DATE: 2006-05-11

PRIOR APPLICATION NUMBER: 60/805,660

PRIOR FILING DATE: 2006-06-23

PRIOR APPLICATION NUMBER: 60/864,554

PRIOR FILING DATE: 2006-11-06

NUMBER OF SEQ ID NOS: 1576

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1512

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

PCT-US07-68410-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17

1 AGTTGAAATTC 12

## RESULT 367

PCT-US07-68412-1512  
; Sequence 1512, Application PC/TUS0768412  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wanczewitz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: EXPRESSION OF GCGR  
; FILE REFERENCE: CORE0061W013  
; CURRENT APPLICATION NUMBER: PCT/US07/68412  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1512  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
PCT-US07-68412-1512

Query Match 44.0%; Score 8.8; DB 3; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17  
||| ||| |||  
Db 1 AGTTGAAGTTTC 12

## RESULT 368

US-09-229-591-33  
; Sequence 33, Application US/09229591  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR  
; TITLE OF INVENTION: ANTAGONIST OBTAINED FROM A CDNA LIBRARY OF PETAL  
; TITLE OF INVENTION: LIVER-SPLEEN  
; FILE REFERENCE: 20411-743CON1  
; CURRENT APPLICATION NUMBER: US/09/229,591  
; CURRENT FILING DATE: 1999-01-13  
; EARLIER APPLICATION NUMBER: US 09/099,818  
; EARLIER FILING DATE: 1998-06-19  
; EARLIER APPLICATION NUMBER: US 09/082,364  
; EARLIER FILING DATE: 1998-05-20  
; EARLIER APPLICATION NUMBER: US 09/079,909  
; EARLIER FILING DATE: 1998-05-15  
; EARLIER APPLICATION NUMBER: US 09/055,010  
; EARLIER FILING DATE: 1998-04-03  
; EARLIER APPLICATION NUMBER: US 09/034,341  
; EARLIER FILING DATE: 1998-02-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 33  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-229-591-33

Query Match 44.0%; Score 8.8; DB 21; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13  
||| ||| |||  
Db 1 CCACAGGTGAAG 12

## RESULT 369

US-09-523-552-22  
; Sequence 22, Application US/09523552  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Pace, Ann  
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF  
; FILE REFERENCE: 28110/36211  
; CURRENT APPLICATION NUMBER: US/09/523,552  
; CURRENT FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: US 09/457,626  
; EARLIER FILING DATE: 1999-12-08  
; EARLIER APPLICATION NUMBER: US 09/417,455  
; EARLIER FILING DATE: 1999-10-13  
; EARLIER APPLICATION NUMBER: US 09/348,942  
; EARLIER FILING DATE: 1999-07-07  
; EARLIER APPLICATION NUMBER: PCT/US99/04291  
; EARLIER FILING DATE: 1999-04-05  
; EARLIER APPLICATION NUMBER: US 09/287,210  
; EARLIER FILING DATE: 1999-04-05  
; EARLIER APPLICATION NUMBER: US 09/251,370  
; EARLIER FILING DATE: 1999-02-17  
; EARLIER APPLICATION NUMBER: US 09/229,591  
; EARLIER FILING DATE: 1999-01-13  
; EARLIER APPLICATION NUMBER: US 09/127,698  
; EARLIER FILING DATE: 1998-07-31  
; EARLIER APPLICATION NUMBER: US 09/099,818  
; EARLIER FILING DATE: 1998-06-19  
; EARLIER APPLICATION NUMBER: US 09/082,364  
; EARLIER FILING DATE: 1998-05-20  
; EARLIER APPLICATION NUMBER: US 09/079,909  
; EARLIER FILING DATE: 1998-05-15  
; EARLIER APPLICATION NUMBER: US 09/055,010  
; EARLIER FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Exon  
US-09-523-552-22

Query Match 44.0%; Score 8.8; DB 24; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13  
||| ||| |||  
Db 1 CCACAGGTGAAG 12

## RESULT 370

US-10-004-382-22  
; Sequence 22, Application US/10004382  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K.

APPLICANT: Haley-Vicente, Dana A.  
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF  
; FILE REFERENCE: 28110/36884A  
; CURRENT APPLICATION NUMBER: US/10/004,382  
; CURRENT FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: US 60/244,692  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Splice Acceptor Site  
US-10-004-382-22

Query Match 44.0%; Score 8.8; DB 38; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCACAGTTGAAG 13  
Db 1 CCACAGGTGAAG 12

RESULT 371  
US-10-257-017B-275104/c  
; Sequence 275104, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 275104  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003785  
US-10-257-017B-275104

Query Match 44.0%; Score 8.8; DB 40; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12  
Db 12 GCCCCACTTTAA 1

RESULT 372  
US-10-257-017B-290891  
; Sequence 290891, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 290891  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014559  
US-10-257-017B-290891

Query Match 44.0%; Score 8.8; DB 40; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTGC 17  
Db 1 AGTTGATGTAGC 12

RESULT 373  
US-10-257-017B-317181/c  
; Sequence 317181, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 317181  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027856  
US-10-257-017B-317181

Query Match 44.0%; Score 8.8; DB 40; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCG 19  
Db 12 TTGAAGTTGCCG 1

RESULT 374  
US-10-257-017B-322885  
; Sequence 322885, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 322885  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031095  
US-10-257-017B-322885

Query Match 44.0%; Score 8.8; DB 40; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17  
||| ||||| |||  
Db 1 AGTAGAAGTTGC 12

RESULT 375  
US-10-257-017B-323132/c  
; Sequence 323132, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 323132  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031232  
US-10-257-017B-323132

Query Match 44.0%; Score 8.8; DB 40; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCGAGTTGAA 12  
||| ||||| |||  
Db 12 GCGCGAGTTGAA 1

RESULT 376  
US-10-257-017B-326883  
; Sequence 326883, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 326883  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033322  
US-10-257-017B-326883

Query Match 44.0%; Score 8.8; DB 40; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20  
||| ||||| |||  
Db 1 TGAGTTGTCT 12

RESULT 377  
US-10-257-017B-327149/c  
; Sequence 327149, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 327149  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033464  
US-10-257-017B-327149

Query Match 44.0%; Score 8.8; DB 40; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20  
||| ||||| |||  
Db 12 TGAAGTTGTCT 1

RESULT 378  
US-10-257-017B-344782  
; Sequence 344782, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 344782  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043703  
US-10-257-017B-344782

Query Match 44.0%; Score 8.8; DB 40; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17  
||| ||||| |||  
Db 1 AGTTGAGATTGC 12

RESULT 379

```
US-10-257-017B-353467
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10257017B
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10257017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353467
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048527
US-10-257-017B-353467

Query Match      44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 1 TGAAGTGGACGT 12

RESULT 380
US-10-257-017B-358049/C
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10257017B
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10257017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358049
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050929
US-10-257-017B-358049

Query Match      44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 12 TGAAGTGGACGT 1

RESULT 381
US-10-257-017B-369872
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10257017B
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
US-10-257-017B-369872
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10257017B
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10257017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369872
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057857
US-10-257-017B-369872

Query Match      44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
DB 1 AGTTGAGTTTC 12

RESULT 382
US-10-257-017B-373811
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10257017B
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10257017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 373811
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060333
US-10-257-017B-373811

Query Match      44.0%; Score 8.8; DB 40; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
DB 1 AGTTGATTTTC 12

RESULT 383
US-10-477-086-15
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE
; FILE REFERENCE: UMB-01-032
; CURRENT APPLICATION NUMBER: US/10477086
; APPLICANT: GONG, Da-Wei
; APPLICANT: SCHULDINER, Alan
; APPLICANT: YANG, Rongze
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE
; FILE REFERENCE: UMB-01-032
; CURRENT APPLICATION NUMBER: US/10477086
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 60/290,829
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: PCT/US02/15103
; PRIOR FILING DATE: 2002-05-14
```

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; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 3'clip
; LOCATION: (1)..(12)
; OTHER INFORMATION: ALt2 Exon 3, intron/exon junction, 3' splice acceptor
US-10-477-086-15

Query Match      44.0%; Score 8.8; DB 47; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTCGAAG 13
Db 1 CCCAGGTGATG 12

RESULT 384
US-10-591-442-27/c
; Sequence 27, Application US/10591442
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-27

Query Match      44.0%; Score 8.8; DB 48; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1

RESULT 385
US-10-591-442-29/c
; Sequence 29, Application US/10591442
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-29

Query Match      44.0%; Score 8.8; DB 48; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1
```

```
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 3'clip
; LOCATION: (1)..(12)
; OTHER INFORMATION: ALt2 Exon 3, intron/exon junction, 3' splice acceptor
US-10-477-086-15

Query Match      44.0%; Score 8.8; DB 47; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTCGAAG 13
Db 1 CCCAGGTGATG 12

RESULT 384
US-10-591-442-27/c
; Sequence 27, Application US/10591442
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-27

Query Match      44.0%; Score 8.8; DB 48; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1

RESULT 385
US-10-591-442-29/c
; Sequence 29, Application US/10591442
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-29

Query Match      44.0%; Score 8.8; DB 48; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1

RESULT 386
US-10-591-442-45/c
; Sequence 45, Application US/10591442
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-45

Query Match      44.0%; Score 8.8; DB 48; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGTTGAACCTG 1

RESULT 387
US-10-708-952A-111659/c
; Sequence 111659, Application US/10708952A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; FILE REFERENCE: 55035
; CURRENT APPLICATION NUMBER: US/10/708,952A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399737
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111659
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Human adenovirus E
; OTHER INFORMATION:
US-10-708-952A-111659

Query Match      44.0%; Score 8.8; DB 51; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
Db 12 TGAGTTGCTGT 1

RESULT 388
US-10-708-952A-289071/c
; Sequence 289071, Application US/10708952A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
```



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; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55035
; CURRENT APPLICATION NUMBER: US/10/708,952A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399737
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 289071
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Human adenovirus E
US-10-708-952A-289071

Query Match      44.0%; Score 8.8; DB 51; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGAGTTGCTGT 1

RESULT 389
US-10-708-952B-111659/c
; Sequence 111659, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111659
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Human adenovirus E
US-10-708-952B-111659

Query Match      44.0%; Score 8.8; DB 51; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGAGTTGCTGT 1

RESULT 390
US-10-708-952B-289071/c
; Sequence 289071, Application US/10708952B
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY VIRAL
; TITLE OF INVENTION: AND VIRAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 06087.0301.CPUS00
; CURRENT APPLICATION NUMBER: US/10/708,952B
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 399738
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 289071
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Human adenovirus E
US-10-708-952B-289071

Query Match      44.0%; Score 8.8; DB 51; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGAGTTGCTGT 1
```

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Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGAGTTGCTGT 1

RESULT 391
US-10-708-953-391440
; Sequence 391440, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 391440
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-391440

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTT 15
Db 1 CCUGUUGAAGCU 12

RESULT 392
US-10-708-953-426502/c
; Sequence 426502, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 426502
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-426502

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGCAGTGGCCGT 1

RESULT 393
US-10-708-953-448734/c
; Sequence 448734, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
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; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 448734
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-448734

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTGAAGTTGCCG 19
Db      12 TTGAAGTTTCAG 1

RESULT 394
US-10-708-953-451057/c
; Sequence 451057, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 451057
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-451057

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGAAGAAGCC 1

RESULT 395
US-10-708-953-467798/c
; Sequence 467798, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 467798
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-467798

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTGCC 18
Db      12 GTTGAAGAAGCC 1

RESULT 396
US-10-708-953-524180/c
; Sequence 524180, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 524180
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-524180

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAA 12
Db      12 GCCCCTGATGAA 1

RESULT 397
US-10-708-953-580776
; Sequence 580776, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 580776
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-580776

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCCCCAGTTGAA 12
Db      1 GCCUCAUUGAA 12

RESULT 398
US-10-708-953-752554
; Sequence 752554, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 752554
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-752554
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US-10-708-953-752554
Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAA 12
   ||||| :|||
Db 1 GCCCUAUUGAA 12

RESULT 399
US-10-708-953-770756
; Sequence 770756, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 770756
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-770756
Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCAGTTCAAGTT 15
   ||||| :
Db 1 CCUGUGAAGCU 12

RESULT 400
US-10-708-953-787100/c
; Sequence 787100, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 787100
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-787100
Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAA 12
   ||||| :|||
Db 12 GCCCCTGATGAA 1

RESULT 401
US-10-708-953-863477/c
; Sequence 863477, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 863477
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-863477
Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
   ||||| :|||
Db 12 TGCAGTGGCCGT 1

RESULT 402
US-10-708-953-924430/c
; Sequence 924430, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 924430
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-924430
Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19
   ||||| :|||
Db 12 TTGAAGTTTCAG 1

RESULT 403
US-10-708-953-925708/c
; Sequence 925708, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 925708
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-925708
Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 9 TGAAGTTGCCGT 20
Db 12 TCAGTGGCCGT 1

RESULT 404
US-10-708-953-958234/c
; Sequence 958234, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 958234
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-958234
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAACCC 1

RESULT 405
US-10-708-953-1033680/c
; Sequence 1033680, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1033680
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1033680
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAACCC 1

RESULT 406
US-10-708-953-1041658
; Sequence 1041658, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1041658
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1041658
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 TGAAGTTGCCGT 20
Db 12 TCAGTGGCCGT 1

RESULT 407
US-10-708-953-1316830/c
; Sequence 1316830, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1316830
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1316830
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CCCAGTTGAAG 13
Db 12 CCCAGGTAAG 1

RESULT 408
US-10-708-953-1342582
; Sequence 1342582, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1342582
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1342582
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CAGTTGAAGTTG 16
Db 1 CAUUUGAACUUG 12

RESULT 409
US-10-708-953-1342582
; Sequence 1342582, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1342582
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-1342582
Query Match 44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CAGTTGAAGTTG 16
Db 1 CAUUUGAACUUG 12
```

## RESULT 409

US-10-708-953-1378924  
; Sequence 1378924, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1378924  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-1378924

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 58.3%; Pred. No. 1.6e+07;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 4 CCAGTTGAAGTT 15  
| | | | | | | | | | | | | |  
Db 1 CCUGUGAAGCU 12

## RESULT 410

US-10-708-953-1380444/c  
; Sequence 1380444, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1380444  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-1380444

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 8 TTGAAGTTGCCG 19  
| | | | | | | | | | | | | | | | | |  
Db 12 TTGAAGTTTCAG 1

## RESULT 411

US-10-708-953-1539333/c  
; Sequence 1539333, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1539333  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-1539333

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 9 TGAAGTTGCCGT 20  
| | | | | | | | | | | | | | | | | |  
Db 12 TGCAGTGGCGT 1

## RESULT 412

US-10-708-953-1669231/c  
; Sequence 1669231, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1669231  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-1669231

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7 GTTGAAGTTGCC 18  
| | | | | | | | | | | | | | | | | |  
Db 12 GTTGAAGAAGCC 1

## RESULT 413

US-10-708-953-1754748/c  
; Sequence 1754748, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1754748  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-1754748

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 CAGTTGAAGTTG 16  
| | | | | | | | | | | | | | | | | |  
Db 12 CTGCTGAAGTTG 1

## RESULT 414

US-10-708-953-1858055  
; Sequence 1858055, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY

; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1858055  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-1858055

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 58.3%; Pred. No. 1.6e+07;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTT 15  
Db 1 CCUGUUGAACU 12

## RESULT 415

US-10-708-953-1868045/c  
; Sequence 1868045, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1868045  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-1868045

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAA 12  
Db 12 GCCCCTGATGAA 1

## RESULT 416

US-10-708-953-1886720  
; Sequence 1886720, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1886720  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-1886720

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 50.0%; Pred. No. 1.6e+07;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16  
Db 1 CAUUGAACUUG 12

## RESULT 417

US-10-708-953-2003791  
; Sequence 2003791, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2003791  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-2003791

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 66.7%; Pred. No. 1.6e+07;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAA 12  
Db 1 GCCUCAUUGAA 12

## RESULT 418

US-10-708-953-2054387/c  
; Sequence 2054387, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2054387  
; LENGTH: 12  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-708-953-2054387

Query Match 44.0%; Score 8.8; DB 52; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20  
Db 12 TGCAGTGCCGT 1

## RESULT 419

US-10-708-953-2142733/c  
; Sequence 2142733, Application US/10708953  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: 55036  
; CURRENT APPLICATION NUMBER: US/10/708,953  
; CURRENT FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 2254510  
; SOFTWARE: PatentIn version 3.2

```
; SEQ ID NO 2142733
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2142733

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 12 CCCAGGTAAG 1

RESULT 420
US-10-708-953-2179457/c
; Sequence 2179457, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2179457
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2179457

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAAGCC 1

RESULT 421
US-10-708-953-2206794/c
; Sequence 2206794, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2206794
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2206794

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCG 19
Db 12 TTGAAGTTTCAG 1

RESULT 422
US-10-708-953-2206794/c
; Sequence 2206794, Application US/10708953
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2206794
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953-2206794

Query Match      44.0%; Score 8.8; DB 52; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCG 19
Db 12 TTGAAGTTTCAG 1

RESULT 423
US-10-708-953A-426502/c
; Sequence 426502, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426502
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-426502

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTT 15
Db 1 CCUGUUGAAGCU 12

RESULT 424
US-10-708-953A-448734/c
; Sequence 448734, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 448734
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-448734

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGCAGTGCCGT 1

RESULT 425
US-10-708-953A-448734/c
; Sequence 448734, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 448734
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-448734
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Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCCG 19
Db 12 TTGAAGTTTCAG 1

RESULT 425
US-10-708-953A-451057/c
; Sequence 451057, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 451057
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-451057

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAAGCC 1

RESULT 426
US-10-708-953A-467798/c
; Sequence 467798, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467798
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-467798

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAAGCC 1

RESULT 427
US-10-708-953A-524180/c
; Sequence 524180, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
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; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 524180
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-524180

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 12 GCCCCTGATGAA 1

RESULT 428
US-10-708-953A-580776
; Sequence 580776, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 580776
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-580776

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 1 GCCUCAUUGAA 12

RESULT 429
US-10-708-953A-752554
; Sequence 752554, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 752554
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-752554

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 1 GCCUCAUUGAA 12

RESULT 430
US-10-708-953A-752554
; Sequence 752554, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 752554
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-752554

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
```



```
Db      1  GCCUCAUUGAA 12
      ||| ||| :|||
      ||| ||| :|||

RESULT 430
US-10-708-953A-770756
; Sequence 770756, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 770756
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-770756

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CCAGTTGAAGTT 15
      ||| ||| :|||
      ||| ||| :|||

Db      1  CCUGUUGAAGCU 12
      ||| ||| :|||
      ||| ||| :|||

RESULT 431
US-10-708-953A-787100/C
; Sequence 787100, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 787100
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-787100

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CCAGTTGAAGTT 15
      ||| ||| :|||
      ||| ||| :|||

Db      1  CCUGUUGAAGCU 12
      ||| ||| :|||
      ||| ||| :|||

RESULT 432
US-10-708-953A-863477/C
; Sequence 863477, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 863477

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  GCCCCAGTTGAA 12
      ||| ||| :|||
      ||| ||| :|||

Db      12  GCCCCAGTTGAA 1
      ||| ||| :|||
      ||| ||| :|||

RESULT 433
US-10-708-953A-924430/C
; Sequence 924430, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 924430
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-924430

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8  TTGAAGTTGCCG 19
      ||| ||| :|||
      ||| ||| :|||

Db      12  TTGAAGTTTCAG 1
      ||| ||| :|||
      ||| ||| :|||

RESULT 434
US-10-708-953A-925708/C
; Sequence 925708, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 925708
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-925708

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9  TGAAGTTGCCGT 20
      ||| ||| :|||
      ||| ||| :|||

Db      12  TGAAGTTGCCGT 1
      ||| ||| :|||
      ||| ||| :|||

RESULT 435
US-10-708-953A-958234/C
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; Sequence 958234, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 958234
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-958234

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAGGCC 1

RESULT 436
US-10-708-953A-1033680/c
; Sequence 1033680, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1033680
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1033680

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
Db 12 GCCCCTGATGAA 1

RESULT 437
US-10-708-953A-1041658
; Sequence 1041658, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1041658
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1041658

Query Match      44.0%; Score 8.8; DB 53; Length 12;
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Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCACTTGAAGTT 15
Db 1 CCUGUGAAGCU 12

RESULT 438
US-10-708-953A-1316830/c
; Sequence 1316830, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1316830
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1316830

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCAAGTTGAAG 13
Db 12 CCCCAAGTTAAG 1

RESULT 439
US-10-708-953A-1342582
; Sequence 1342582, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1342582
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1342582

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 50.0%; Pred. No. 1.6e+07;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16
Db 1 CAUUGAAGACUG 12

RESULT 440
US-10-708-953A-1378924
; Sequence 1378924, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
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; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1378924
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1378924

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTT 15
DB 1 CCUGUUGAAGCU 12

RESULT 441
US-10-708-953A-1380444/c
; Sequence 1380444, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1380444
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1380444

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19
DB 12 TTGAAGTTTCAG 1

RESULT 442
US-10-708-953A-1539333/c
; Sequence 1539333, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1539333
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1539333

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 12 TGAAGTTGCCGT 20

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; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1858055

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 58.3%; Pred. No. 1.6e+07;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTT 15
   ||::|||:
Db 1 CCUGUGAAGCU 12

RESULT 446
US-10-708-953A-1868045/c
; Sequence 1868045, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1868045
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1868045

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAA 12
   |||||:|
Db 12 GCCCCTGATGAA 1

RESULT 447
US-10-708-953A-1886720
; Sequence 1886720, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1886720
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-1886720

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 50.0%; Pred. No. 1.6e+07;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTG 16
   ||::|||:|
Db 1 CAUUGAACUUG 12

RESULT 448
US-10-708-953A-2003791
; Sequence 2003791, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2003791
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2003791

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 66.7%; Pred. No. 1.6e+07;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAA 12
   |||||:|
Db 1 GCCUCAUUGAA 12

RESULT 449
US-10-708-953A-2054387/c
; Sequence 2054387, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2054387
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2054387

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
   |||||:|
Db 12 TGCAGTGCCGT 1

RESULT 450
US-10-708-953A-2142733/c
; Sequence 2142733, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2142733
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2142733

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
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; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190034
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-190034

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCAGTTGAAG 13
Db 12 CCCAGGTGAAG 1

RESULT 451
US-10-708-953A-2179457/c
; Sequence 2179457, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2179457
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2179457

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCC 18
Db 12 GTTGAAGAGCC 1

RESULT 452
US-10-708-953A-2206794/c
; Sequence 2206794, Application US/10708953A
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 55036
; CURRENT APPLICATION NUMBER: US/10/708,953A
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 2254510
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2206794
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-953A-2206794

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TTGAAGTTGCG 19
Db 12 TTGAAGTTGAG 1

RESULT 453
US-10-709-572-190034/c
; Sequence 190034, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 258617
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-258617

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGAAGTTGCCGT 20
Db 12 TGAAGCTGCTGT 1

RESULT 455
US-10-709-572-258617
; Sequence 258617, Application US/10709572
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; FILE REFERENCE: 050992.0202.CPUS01
; CURRENT APPLICATION NUMBER: US/10/709,572
; CURRENT FILING DATE: 2005-05-14
; NUMBER OF SEQ ID NOS: 10068324
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 258617
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-709-572-258617

Query Match      44.0%; Score 8.8; DB 53; Length 12;
Score over Length 73.3%;
```

; ;

Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCAGTTGAA 12  
||| ||| ||| |||  
Db 1 GCTCCAGTGGAA 12

## RESULT 456

US-10-709-572-260004/c  
; Sequence 260004, Application US/10709572  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Amiel, Amir  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY  
; FILE REFERENCE: OLIGONUCLEOTIDES AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10/709,572  
; CURRENT FILING DATE: 2005-05-14  
; NUMBER OF SEQ ID NOS: 10068324  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 260004  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-709-572-260004

Query Match 44.0%; Score 8.8; DB 53; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTGAAGTTGCCG 19  
||||| ||| |||  
Db 12 TTGAAGTTGCAG 1

## RESULT 457

US-11-126-421-15  
; Sequence 15, Application US/11126421  
; GENERAL INFORMATION:  
; APPLICANT: GONG, Da-Wei  
; APPLICANT: SCHULDNER, Alan  
; APPLICANT: YANG, Rongze  
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE  
; FILE REFERENCE: UMB-01-032  
; CURRENT APPLICATION NUMBER: US/11/126,421  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US/10/477,086  
; PRIOR FILING DATE: 2003-11-06  
; PRIOR APPLICATION NUMBER: US 60/250,829  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: PCT/US02/15103  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 15  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: 3'clip  
; LOCATION: (1)..(12)  
; OTHER INFORMATION: ALT2 Exon 3, intron/exon junction, 3' splice acceptor  
US-11-126-421-15

Query Match 44.0%; Score 8.8; DB 66; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13

Db 1 CCCAGGTGATG 12  
||||| ||| |

## RESULT 458

US-11-438-135-357  
; Sequence 357, Application US/11438135  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Gingeras, Thomas R.  
; APPLICANT: Huang, Xiaohua C.  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Garrett Miyada, Charles  
; APPLICANT: Morris, Macdonald S.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
; TITLE OF INVENTION: Biological Chips  
; NUMBER OF SEQUENCES: 585  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: 2 Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/438,135  
; FILING DATE: 19-MAY-2006  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/510,521  
; FILING DATE: 02-Aug-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/12305  
; FILING DATE: 26-OCT-1994  
; APPLICATION NUMBER: US 08/284,064  
; FILING DATE: 02-AUG-1994  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebescheutz, Joe  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004120US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 357:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
US-11-438-135-357

Query Match 44.0%; Score 8.8; DB 75; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20  
||||| ||| |||  
Db 1 TGGAGTTGCAGT 12

RESULT 459  
US-11-438-135-358  
; Sequence 358, Application US/11438135  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Ginteras, Thomas R.  
; APPLICANT: Huang, Xiaohua C.  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Lipshutz, Robert E.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
; TITLE OF INVENTION: Biological Chips  
; NUMBER OF SEQUENCES: 585  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: 2 Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/438,135  
; FILING DATE: 19-MAY-2006  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/510,521  
; FILING DATE: 02-Aug-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/12305  
; FILING DATE: 26-OCT-1994  
; APPLICATION NUMBER: US 08/284,064  
; FILING DATE: 02-AUG-1994  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebescheutz, Joe  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004120US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 358:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
US-11-438-135-358

Query Match 44.0%; Score 8.8; DB 75; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 6 AGTTGAAGTTGC 17  
Db 1 ATTTGAGTTGC 12

RESULT 460  
US-11-585-939A-7/c

; Sequence 7, Application US/11585939A  
; GENERAL INFORMATION:  
; APPLICANT: HAYASHI, Miho  
; APPLICANT: MORI, Kazuyoshi  
; APPLICANT: MAEDA, Mizuo  
; TITLE OF INVENTION: DNA SEPARATION DEVICE, DNA SEPARATION METHOD, AND LIGAND DNA  
; FILE REFERENCE: 2006\_1956A  
; CURRENT APPLICATION NUMBER: US/11/585,939A  
; CURRENT FILING DATE: 2006-10-25  
; PRIOR APPLICATION NUMBER: JP 2005-311933  
; PRIOR FILING DATE: 2005-10-26  
; NUMBER OF SEQ ID NOS: 15  
; SEQ ID NO 7  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-585-939A-7  
Query Match 44.0%; Score 8.8; DB 78; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 CCCGAGTTGAAG 13  
Db 12 CCCGAGCCGAAG 1  
RESULT 461  
US-11-745-429-1512  
; Sequence 1512, Application US/11745429  
; GENERAL INFORMATION:  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Richard S. Geary  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Punit P. Seth  
; APPLICANT: Andrew M. Siwkowski  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Edward Wanciewicz  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: GENE EXPRESSION  
; FILE REFERENCE: CORE0061US7  
; CURRENT APPLICATION NUMBER: US/11/745,429  
; CURRENT FILING DATE: 2007-05-25  
; PRIOR APPLICATION NUMBER: PCT/US2007/061183  
; PRIOR FILING DATE: 2007-01-27  
; PRIOR APPLICATION NUMBER: 60/746,631  
; PRIOR FILING DATE: 2006-05-05  
; PRIOR APPLICATION NUMBER: 60/747,059  
; PRIOR FILING DATE: 2006-05-11  
; PRIOR APPLICATION NUMBER: 60/805,660  
; PRIOR FILING DATE: 2006-06-23  
; PRIOR APPLICATION NUMBER: 60/864,554  
; PRIOR FILING DATE: 2006-11-06  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1512  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-11-745-429-1512  
Query Match 44.0%; Score 8.8; DB 81; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 1.6e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 6 AGTTGAAGTTGC 17  
Db 1 AGTTGAATTC 12

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; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Splice Acceptor Site
US-60-244-692-22

Query Match      44.0%; Score 8.8; DB 87; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCAGTTGAAG 13
Db 1 CCACAGTGAAG 12

RESULT 464
US-09-546-745A-4860/c
; Sequence 4860, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4860
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-4860

Query Match      62.0%; Score 12.4; DB 25; Length 17;
Score over Length 72.9%;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTC 17
Db 16 CCAGTTGAAGTTC 3

RESULT 465
US-09-546-745A-4861/c
; Sequence 4861, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
```

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; PRIOR APPLICATION NUMBER: US/11/799,117
; PRIOR FILING DATE: 2007-05-01
; PRIOR APPLICATION NUMBER: 11/595,485
; PRIOR FILING DATE: 2006-11-10
; PRIOR APPLICATION NUMBER: 60/862,350
; PRIOR FILING DATE: 2006-10-20
; PRIOR APPLICATION NUMBER: 60/735,429
; PRIOR FILING DATE: 2005-11-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-799-117-48

Query Match      44.0%; Score 8.8; DB 81; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 1.6e+07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCCCAGTTGAA 12
Db 12 GACCCAGGTGAA 1

RESULT 463
US-60-244-692-22
; Sequence 22, Application US/60244692
; GENERAL INFORMATION:
; APPLICANT: Mize, Nancy K.
; APPLICANT: Haley-Vicente, Dana A.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36884
; CURRENT APPLICATION NUMBER: US/60/244,692
; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: PCT/US00/18710
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/576,008
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/523,552
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/457,626
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
```



```
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4861
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-4861

Query Match      62.0%; Score 12.4; DB 25; Length 17;
Score over Length 72.9%;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCAGTTGAAGTTGC 17
Db 15 CCAGTTGAAGTTGC 2

RESULT 466
US-10-605-923-508977
; Sequence 508977, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 508977
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-508977

Query Match      62.0%; Score 12.4; DB 49; Length 17;
Score over Length 72.9%;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGTTG 16
Db 1 CCCAGTTGAAGATG 14

RESULT 467
PCT-US05-37925-39/c
; Sequence 39, Application PC/TUS0537925
; GENERAL INFORMATION:
; APPLICANT: Hitachi Chemical Co., Ltd.
; APPLICANT: Hitachi Chemical Research Center, Inc
; APPLICANT: MITSUHASHI, Masato
; TITLE OF INVENTION: METHOD FOR TAILORING ADMINISTRATION OF
; TITLE OF INVENTION: DRUGS BY QUANTITATION OF mRNA
; FILE REFERENCE: HITACHI.066VPC
; CURRENT APPLICATION NUMBER: PCT/US05/37925
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/620,603
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/653,557
; PRIOR FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: 60/688,741
; PRIOR FILING DATE: 2005-06-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence

Query Match      62.0%; Score 16; DB 3; Length 22;
Score over Length 72.7%;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 468
PCT-US05-37925-51/c
; Sequence 51, Application PC/TUS0537925
; GENERAL INFORMATION:
; APPLICANT: Hitachi Chemical Co., Ltd.
; APPLICANT: Hitachi Chemical Research Center, Inc
; APPLICANT: MITSUHASHI, Masato
; TITLE OF INVENTION: METHOD FOR TAILORING ADMINISTRATION OF
; TITLE OF INVENTION: DRUGS BY QUANTITATION OF mRNA
; FILE REFERENCE: HITACHI.066VPC
; CURRENT APPLICATION NUMBER: PCT/US05/37925
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/620,603
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/653,557
; PRIOR FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: 60/688,741
; PRIOR FILING DATE: 2005-06-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer sequence
PCT-US05-37925-51

Query Match      80.0%; Score 16; DB 3; Length 22;
Score over Length 72.7%;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20
Db 22 CAGTTGAAGTTGCCGT 7

RESULT 469
PCT-US06-00086-6/c
; Sequence 6, Application PC/TUS0600086
; GENERAL INFORMATION:
; APPLICANT: Murakami, Taku
; TITLE OF INVENTION: PRIMER GENERATION ROLLING CIRCLE
; TITLE OF INVENTION: AMPLIFICATION
; FILE REFERENCE: HITACHI.067VPC
; CURRENT APPLICATION NUMBER: PCT/US06/00086
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US 60/641,255
; PRIOR FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically prepared oligonucleotide sequence
PCT-US06-00086-6
```

Query Match 80.0%; Score 16; DB 3; Length 22;  
Score over Length 72.7%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20  
|||||  
Db 22 CAGTTGAAGTTGCCGT 7

## RESULT 470

US-10-605-923-810848  
; Sequence 810848, Application US/10605923  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND  
; FILE OF INVENTION: US5 THEREOF  
; FILE REFERENCE: 55000  
; CURRENT APPLICATION NUMBER: US/10/605,923  
; CURRENT FILING DATE: 2003-11-06  
; NUMBER OF SEQ ID NOS: 1515668  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 810848  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-605-923-810848

Query Match 69.0%; Score 13.8; DB 49; Length 19;  
Score over Length 72.6%;  
Best Local Similarity 88.2%; Pred. No. 4.9e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTTGCC 18  
|||  
Db 3 CCACATTTGAAGTTGCC 19

## RESULT 471

US-10-605-924-801404/c  
; Sequence 801404, Application US/10605924  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND  
; FILE OF INVENTION: US5 THEREOF  
; FILE REFERENCE: 55004  
; CURRENT APPLICATION NUMBER: US/10/605,924  
; CURRENT FILING DATE: 2003-11-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 801404  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-605-924-801404

Query Match 69.0%; Score 13.8; DB 50; Length 19;  
Score over Length 72.6%;  
Best Local Similarity 88.2%; Pred. No. 4.9e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAGTTGCC 18  
|||  
Db 17 CCACATTTGAAGTTGCC 1

## RESULT 472

US-09-528-209A-6207  
; Sequence 6207, Application US/09528209A  
; GENERAL INFORMATION:  
; APPLICANT: Agilent Technologies  
; TITLE OF INVENTION: Computational Method for Constructing a Universal

; TITLE OF INVENTION: Tag-Antitag Molecular Array System for Hybridization  
; FILE REFERENCE: 10992790  
; CURRENT APPLICATION NUMBER: US/09/528,209A  
; CURRENT FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 10286  
; SOFTWARE: Bergstrom Sequence Formatter  
; SEQ ID NO 6207  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A tag sequence incorporated in a probe nucleotide, the tag  
; OTHER INFORMATION: sequence complementary to an antitag sequence incorporated  
; OTHER INFORMATION: within a universal tag-antitag molecular array  
US-09-528-209A-6207

Query Match 47.0%; Score 9.4; DB 24; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 8.1e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 3 AGTTGAAGATG 13

## RESULT 473

US-10-257-017B-6223  
; Sequence 6223, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 6223  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001948  
US-10-257-017B-6223

Query Match 47.0%; Score 9.4; DB 40; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 8.1e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 3 AGTAGAAGTTG 13

## RESULT 474

US-10-257-017B-6224/c  
; Sequence 6224, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
US-10-257-017B-6224/c

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 6224
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001948
US-10-257-017B-6224

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      11 AGTAGAAGTTG 1

RESULT 475
US-10-257-017B-12629
; Sequence 12629, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12629
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002968
US-10-257-017B-12629

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      2 AGTTGATGTTG 12

RESULT 476
US-10-257-017B-12630/c
; Sequence 12630, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12630
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002968
US-10-257-017B-12630/c

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      2 AGTTGATGTTG 12

RESULT 477
US-10-257-017B-25055
; Sequence 25055, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25055
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25055

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 TGAAGTTGCCG 19
Db      3 TGAAGTTGCCG 13

RESULT 478
US-10-257-017B-25056/c
; Sequence 25056, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25056
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25056

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002968
US-10-257-017B-12630

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      12 AGTTGATGTTG 2

RESULT 477
US-10-257-017B-25055
; Sequence 25055, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25055
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25055

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 TGAAGTTGCCG 19
Db      3 TGAAGTTGCCG 13

RESULT 478
US-10-257-017B-25056/c
; Sequence 25056, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25056
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25056

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 9 TGAAGTTGCG 19
Db 11 TGAAGTTGCG 1

RESULT 479
US-10-257-017B-25081
; Sequence 25081, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25081
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00006096
US-10-257-017B-25081
Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 2 AGTGAAGTTG 12

RESULT 480
US-10-257-017B-25082/c
; Sequence 25082, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25082
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00006096
US-10-257-017B-25082
Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 12 AGTGAAGTTG 2

RESULT 481
US-10-257-017B-25082/c
; Sequence 25082, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25082
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00007879
US-10-257-017B-25082
Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 13 AGTTGAAGTTG 3

RESULT 483
US-10-257-017B-36537
; Sequence 36537, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
US-10-257-017B-27969
; Sequence 27969, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 27969
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00007879
US-10-257-017B-27969
Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 1 AGTTGAAGTTG 11

RESULT 482
US-10-257-017B-27970/c
; Sequence 27970, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 27970
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00007879
US-10-257-017B-27970
Query Match 47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
Db 13 AGTTGAAGTTG 3

RESULT 483
US-10-257-017B-36537
; Sequence 36537, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 36537
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011456
US-10-257-017B-36537

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
DB      1 ATTGGAAGTTG 11

RESULT 484
US-10-257-017B-36538/c
; Sequence 36538, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 36538
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011456
US-10-257-017B-36538

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
DB      13 ATTGGAAGTTG 3

RESULT 485
US-10-257-017B-56753
; Sequence 56753, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 56753
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56753

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
DB      1 AGTTGAATTTG 11

RESULT 486
US-10-257-017B-56754/c
; Sequence 56754, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 56754
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56754

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
DB      13 AGTTGAATTTG 3

RESULT 487
US-10-257-017B-96965
; Sequence 96965, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96965
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054
US-10-257-017B-96965
```

Query Match 47.0%; Score 9.4; DB 40; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 8.1e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19  
|||||  
DB 1 TGAAGTTGCCG 11

RESULT 488  
US-10-257-017B-96966/c  
; Sequence 96966, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 96966  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054  
US-10-257-017B-96966

Query Match 47.0%; Score 9.4; DB 40; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 8.1e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19  
|||||  
DB 13 TGAAGTTGCCG 3

RESULT 489  
US-10-257-017B-111321  
; Sequence 111321, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 111321  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809  
US-10-257-017B-111321

Query Match 47.0%; Score 9.4; DB 40; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 8.1e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16

Db 3 AGTTGATGTTG 13  
|||||

RESULT 490  
US-10-257-017B-111322/c  
; Sequence 111322, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 111322  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809  
US-10-257-017B-111322

Query Match 47.0%; Score 9.4; DB 40; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 8.1e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
DB 11 AGTTGATGTTG 1

RESULT 491  
US-10-257-017B-117287  
; Sequence 117287, Application US/10257017B  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 117287  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029345  
US-10-257-017B-117287

Query Match 47.0%; Score 9.4; DB 40; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 8.1e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
DB 3 AGTTGATGTTG 13

RESULT 492  
US-10-257-017B-117288/c  
; Sequence 117288, Application US/10257017B

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117288
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029345
US-10-257-017B-117288

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      11 AGTTGTAAGTTG 1

RESULT 493
US-10-257-017B-117509
; Sequence 117509, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117509
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029385
US-10-257-017B-117509

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      3 AGTTGAAATTG 13

RESULT 494
US-10-257-017B-117510/c
; Sequence 117510, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117510
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029385
US-10-257-017B-117510

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      11 AGTTGAAATTG 1

RESULT 495
US-10-257-017B-187027
; Sequence 187027, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187027
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187027

Query Match          47.0%; Score 9.4; DB 40; Length 13;
Score over Length    72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTTG 16
Db      1 AGTTGAAAGTTG 11

RESULT 496
US-10-257-017B-187028/c
; Sequence 187028, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187028
; LENGTH: 13
```

```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187028

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3

RESULT 497
US-10-257-017B-215785
/ Sequence 215785, Application US/10257017B
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 215785
/ LENGTH: 13
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052481
US-10-257-017B-215785

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 11

RESULT 498
US-10-257-017B-215786/c
/ Sequence 215786, Application US/10257017B
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 215786
/ LENGTH: 13
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052481
US-10-257-017B-215786

Query Match      47.0%; Score 9.4; DB 40; Length 13;
```

```
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3

RESULT 499
US-10-257-017B-235787
/ Sequence 235787, Application US/10257017B
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 235787
/ LENGTH: 13
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
US-10-257-017B-235787

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 11

RESULT 500
US-10-257-017B-235788/c
/ Sequence 235788, Application US/10257017B
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 235788
/ LENGTH: 13
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
US-10-257-017B-235788

Query Match      47.0%; Score 9.4; DB 40; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 8.1e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAAGTTG 3
```



Search completed: December 3, 2007, 22:10:54  
Job time : 17732 secs

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 17:42:58 ; Search time 337 Seconds  
(without alignments)  
44,536 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccccagtggaagttgccgt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 614577 seqs, 375217992 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 12

Maximum DB seq length: 30

Post-processing: Minimum Score over Length 70%

Listing first 1000 summaries

Database : Pending Patents NA New:\*

- 1: /EMC\_Celerra\_SIDS2/ptodata/2/pna/PCT\_NEW\_COMB.seq.\*
- 2: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US05\_NEW\_COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US07\_NEW\_COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US08\_NEW\_COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US09\_NEW\_COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US10\_NEW\_COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US11\_NEW\_COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS2/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Length	Match	Query over	DB ID	Description
C 1	16	72.7	80.0	22	1	PCT-US07-11121-41 Sequence 4

ALIGNMENTS

RESULT 1  
PCT-US07-11121-41/c  
; Sequence 41, Application PC/TUS0711121  
; GENERAL INFORMATION:  
; APPLICANT: Hitachi Chemical Co., Ltd.  
; APPLICANT: Hitachi Chemical Research Center, Inc.  
; APPLICANT: Mitsuhashi, Masato  
; APPLICANT: Ibara, Kazuhiko  
; TITLE OF INVENTION: Method for Testing Drug Sensitivity in Solid Tumors by Quantifying mRNA Expression in Thinly-Sliced Tumor Tissue  
; TITLE OF INVENTION: Tumor Tissue  
; FILE REFERENCE: HITACHI.081VPC  
; CURRENT APPLICATION NUMBER: PCT/US07/11121  
; PRIOR FILING DATE: 2007-09-19  
; PRIOR APPLICATION NUMBER: PCT/US2007/011121  
; PRIOR FILING DATE: 2007-05-08  
; PRIOR APPLICATION NUMBER: US 60/798,674  
; PRIOR FILING DATE: 2006-05-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 41  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: BAX forward primer sequence  
PCT-US07-11121-41

Query Match 80.0%; Score 16; DB 1; Length 22;  
Score over Length 72.7%;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGTTGAAGTTGCCGT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 22 CAGTTGAAGTTGCCGT 7

Search completed: December 3, 2007, 17:52:03  
Job time : 337 secs

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2007, 17:46:50 ; Search time 1293 Seconds

(without alignment)

367.071 Million cell updates/sec

Title: US-10-728-509-64

Perfect score: 20

Sequence: 1 gccacgttgagttgccgt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0.

Searched: 31364175 seqs, 1186555624 residues

Total number of hits satisfying chosen parameters: 308

Minimum DB seq length: 12

Maximum DB seq length: 30

Post-processing: Minimum Score over Length 70%

Listing first 1000 summaries

Database : Published Applications NA Main:\*

1:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
6:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US09D_PUBCOMB.seq.*
7:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
8:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
9:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
10:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
11:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
12:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
13:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
14:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
15:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
16:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10J_PUBCOMB.seq.*
17:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US10K_PUBCOMB.seq.*
18:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
19:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11B_PUBCOMB.seq.*
20:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11C_PUBCOMB.seq.*
21:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11D_PUBCOMB.seq.*
22:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11E_PUBCOMB.seq.*
23:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11F_PUBCOMB.seq.*
24:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11G_PUBCOMB.seq.*
25:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11H_PUBCOMB.seq.*
26:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11I_PUBCOMB.seq.*
27:	/EMC_Celerra_SIDS2/ptodata/1/pubpna/US11J_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score over		Query Match	Length	DB	ID	Description
	Score	%					
1	20	100.0	100.0	20	3	US-09-908-147-64	Sequence 6
2	20	100.0	100.0	20	9	US-10-728-509-64	Sequence 6
3	18	90.0	90.0	20	3	US-09-908-147-65	Sequence 6
4	18	90.0	90.0	20	9	US-10-728-509-65	Sequence 6
5	15	83.3	75.0	18	3	US-09-908-147-5	Sequence 5
6	15	83.3	75.0	18	9	US-10-728-509-5	Sequence 5
7	10	83.3	50.0	12	10	US-10-257-017B-271773	Sequence 2

12	10	US-10-257-017B-274756	Sequence 2
12	10	US-10-257-017B-310208	Sequence 3
12	10	US-10-257-017B-341473	Sequence 3
12	10	US-10-257-017B-353251	Sequence 3
12	10	US-10-257-017B-355811	Sequence 3
20	3	US-09-908-147-119	Sequence 1
20	3	US-10-728-509-119	Sequence 1
14	2	US-08-591-4868-33	Sequence 3
14	11	US-10-984-919-857	Sequence 8
15	9	US-10-138-674-4126	Sequence 4
15	9	US-10-287-949A-4126	Sequence 4
15	11	US-10-951-303-4126	Sequence 4
15	23	US-11-088-219-4126	Sequence 4
13	10	US-10-257-017B-187031	Sequence 1
13	10	US-10-257-017B-187032	Sequence 1
17	27	US-11-495-951A-94101	Sequence 9
12	10	US-10-257-017B-275133	Sequence 2
12	10	US-10-257-017B-280261	Sequence 2
12	10	US-10-257-017B-281972	Sequence 2
12	10	US-10-257-017B-282569	Sequence 2
12	10	US-10-257-017B-300630	Sequence 3
12	10	US-10-257-017B-305246	Sequence 3
12	10	US-10-257-017B-314348	Sequence 3
12	10	US-10-257-017B-329434	Sequence 3
12	10	US-10-257-017B-337757	Sequence 3
12	10	US-10-257-017B-339358	Sequence 3
12	10	US-10-257-017B-345090	Sequence 3
12	10	US-10-257-017B-361423	Sequence 3
13	10	US-10-257-017B-28743	Sequence 2
13	10	US-10-257-017B-28744	Sequence 2
13	10	US-10-257-017B-65609	Sequence 6
13	10	US-10-257-017B-65610	Sequence 6
13	10	US-10-257-017B-107775	Sequence 1
13	10	US-10-257-017B-107776	Sequence 1
13	10	US-10-257-017B-131258	Sequence 1
13	10	US-10-257-017B-131259	Sequence 1
13	10	US-10-257-017B-150111	Sequence 1
13	10	US-10-257-017B-150112	Sequence 1
13	10	US-10-257-017B-153411	Sequence 1
13	10	US-10-257-017B-153412	Sequence 1
13	10	US-10-257-017B-171651	Sequence 1
13	10	US-10-257-017B-171652	Sequence 1
13	21	US-11-051-720-809	Sequence 8
13	22	US-11-043-842-704	Sequence 7
17	17	US-11-495-951A-101428	Sequence 4
17	27	US-11-495-951A-101428	Sequence 4
12	10	US-10-257-017B-272526	Sequence 2
12	10	US-10-257-017B-281370	Sequence 2
12	10	US-10-257-017B-284630	Sequence 2
12	10	US-10-257-017B-288152	Sequence 2
12	10	US-10-257-017B-298602	Sequence 2
12	10	US-10-257-017B-298745	Sequence 2
12	10	US-10-257-017B-299311	Sequence 2
12	10	US-10-257-017B-303341	Sequence 3
12	10	US-10-257-017B-305026	Sequence 3
12	10	US-10-257-017B-307994	Sequence 3
12	10	US-10-257-017B-310012	Sequence 3
12	10	US-10-257-017B-319646	Sequence 3
12	10	US-10-257-017B-332564	Sequence 3
12	10	US-10-257-017B-333972	Sequence 3
12	10	US-10-257-017B-337673	Sequence 3
12	10	US-10-257-017B-338530	Sequence 3
12	10	US-10-257-017B-338626	Sequence 3
12	10	US-10-257-017B-342781	Sequence 3
12	10	US-10-257-017B-343923	Sequence 3
12	10	US-10-257-017B-345821	Sequence 3
12	10	US-10-257-017B-358109	Sequence 3
12	10	US-10-257-017B-360215	Sequence 3
12	10	US-10-257-017B-365894	Sequence 3
12	10	US-10-257-017B-369254	Sequence 3
12	10	US-10-257-017B-369635	Sequence 3
12	10	US-10-257-017B-379943	Sequence 3
12	14	US-09-168-791-14	Sequence 1

C 81	10.4	74.3	52.0	14	10	US-10-799-238-14	Sequence 1	C 154	12	70.6	60.0	17	9	US-10-287-949A-1646	Sequence 1
C 82	9.6	73.8	48.0	13	10	US-10-257-017B-61663	Sequence 6	C 155	12	70.6	60.0	17	9	US-10-287-949A-1647	Sequence 1
C 83	9.6	73.8	48.0	13	10	US-10-257-017B-61664	Sequence 6	C 156	12	70.6	60.0	17	9	US-10-287-949A-6253	Sequence 6
C 84	11.8	73.8	59.0	16	9	US-10-138-674-5807	Sequence 5	C 157	12	70.6	60.0	17	9	US-10-287-949A-6254	Sequence 6
C 85	11.8	73.8	59.0	16	9	US-10-287-949A-5807	Sequence 5	C 158	12	70.6	60.0	17	9	US-10-287-949A-8571	Sequence 8
C 86	11.8	73.8	59.0	16	23	US-11-088-219-5807	Sequence 5	C 159	12	70.6	60.0	17	10	US-10-712-633-3654	Sequence 3
C 87	14	73.7	70.0	19	15	US-10-714-333A-764639	Sequence 7	C 160	12	70.6	60.0	17	11	US-10-951-303-1646	Sequence 1
C 88	14	73.7	70.0	19	15	US-10-714-333A-764639	Sequence 7	C 161	12	70.6	60.0	17	11	US-10-951-303-1647	Sequence 1
C 89	14	73.7	70.0	19	20	US-11-083-784-764639	Sequence 7	C 162	12	70.6	60.0	17	23	US-11-088-219-1646	Sequence 1
C 90	11	73.3	55.0	15	3	US-09-504-231A-1284	Sequence 1	C 163	12	70.6	60.0	17	23	US-11-088-219-1647	Sequence 1
C 91	11	73.3	55.0	15	3	US-09-274-553D-1284	Sequence 1	C 164	12	70.6	60.0	17	23	US-11-088-219-6253	Sequence 6
C 92	11	73.3	55.0	15	9	US-10-138-674-4150	Sequence 4	C 165	12	70.6	60.0	17	23	US-11-088-219-6254	Sequence 6
C 93	11	73.3	55.0	15	9	US-10-287-949A-4150	Sequence 4	C 166	12	70.6	60.0	17	23	US-11-088-219-8571	Sequence 8
C 94	11	73.3	55.0	15	11	US-10-951-303-4150	Sequence 4	C 167	13.4	70.5	67.0	19	12	US-10-310-914A-1191074	Sequence 1
C 95	11	73.3	55.0	15	23	US-11-088-219-4150	Sequence 4	C 168	13.4	70.5	67.0	19	15	US-10-714-333A-726378	Sequence 7
C 96	8.8	73.3	44.0	12	10	US-10-477-086-15	Sequence 1	C 169	13.4	70.5	67.0	19	15	US-10-714-333A-726385	Sequence 7
C 97	8.8	73.3	44.0	12	10	US-10-257-017B-275104	Sequence 2	C 170	13.4	70.5	67.0	19	15	US-10-714-333A-1192689	Sequence 1
C 98	8.8	73.3	44.0	12	10	US-10-257-017B-290891	Sequence 2	C 171	13.4	70.5	67.0	19	15	US-10-714-333A-1192696	Sequence 1
C 99	8.8	73.3	44.0	12	10	US-10-257-017B-317181	Sequence 3	C 172	13.4	70.5	67.0	19	15	US-10-714-333A-1192704	Sequence 1
C 100	8.8	73.3	44.0	12	10	US-10-257-017B-322885	Sequence 3	C 173	13.4	70.5	67.0	19	15	US-11-083-784-726378	Sequence 7
C 101	8.8	73.3	44.0	12	10	US-10-257-017B-323132	Sequence 3	C 174	13.4	70.5	67.0	19	19	US-11-083-784-726385	Sequence 7
C 102	8.8	73.3	44.0	12	10	US-10-257-017B-326883	Sequence 3	C 175	13.4	70.5	67.0	19	19	US-11-083-784-1192689	Sequence 1
C 103	8.8	73.3	44.0	12	10	US-10-257-017B-327149	Sequence 3	C 176	13.4	70.5	67.0	19	19	US-11-083-784-1192696	Sequence 1
C 104	8.8	73.3	44.0	12	10	US-10-257-017B-344782	Sequence 3	C 177	13.4	70.5	67.0	19	19	US-11-083-784-1192704	Sequence 1
C 105	8.8	73.3	44.0	12	10	US-10-257-017B-353467	Sequence 3	C 178	13.4	70.5	67.0	19	20	US-11-101-244-726378	Sequence 7
C 106	8.8	73.3	44.0	12	10	US-10-257-017B-358049	Sequence 3	C 179	13.4	70.5	67.0	19	20	US-11-101-244-726385	Sequence 7
C 107	8.8	73.3	44.0	12	10	US-10-257-017B-369872	Sequence 3	C 180	13.4	70.5	67.0	19	20	US-11-101-244-1192689	Sequence 1
C 108	8.8	73.3	44.0	12	10	US-10-257-017B-373811	Sequence 3	C 181	13.4	70.5	67.0	19	20	US-11-101-244-1192696	Sequence 1
C 109	8.8	73.3	44.0	12	17	US-10-591-442-27	Sequence 2	C 182	13.4	70.5	67.0	19	20	US-11-101-244-1192704	Sequence 1
C 110	8.8	73.3	44.0	12	17	US-10-591-442-29	Sequence 2	C 183	11.2	70.0	56.0	16	17	US-10-535-164-474753	Sequence 4
C 111	8.8	73.3	44.0	12	17	US-10-591-442-45	Sequence 4	C 184	8.4	70.0	42.0	12	7	US-10-078-958-50	Sequence 5
C 112	8.8	73.3	44.0	12	18	US-11-126-421-15	Sequence 1	C 185	8.4	70.0	42.0	12	7	US-10-078-958-59	Sequence 5
C 113	8.8	73.3	44.0	12	27	US-11-585-939A-7	Sequence 7	C 186	8.4	70.0	42.0	12	10	US-10-257-017B-269582	Sequence 2
C 114	13.8	72.6	69.0	19	12	US-10-310-914A-801404	Sequence 8	C 187	8.4	70.0	42.0	12	10	US-10-257-017B-269967	Sequence 2
C 115	9.4	72.3	47.0	13	10	US-10-257-017B-8223	Sequence 6	C 188	8.4	70.0	42.0	12	10	US-10-257-017B-270364	Sequence 2
C 116	9.4	72.3	47.0	13	10	US-10-257-017B-8224	Sequence 6	C 189	8.4	70.0	42.0	12	10	US-10-257-017B-270867	Sequence 2
C 117	9.4	72.3	47.0	13	10	US-10-257-017B-12629	Sequence 1	C 190	8.4	70.0	42.0	12	10	US-10-257-017B-272438	Sequence 2
C 118	9.4	72.3	47.0	13	10	US-10-257-017B-12630	Sequence 1	C 191	8.4	70.0	42.0	12	10	US-10-257-017B-272556	Sequence 2
C 119	9.4	72.3	47.0	13	10	US-10-257-017B-25055	Sequence 2	C 192	8.4	70.0	42.0	12	10	US-10-257-017B-274200	Sequence 2
C 120	9.4	72.3	47.0	13	10	US-10-257-017B-25056	Sequence 2	C 193	8.4	70.0	42.0	12	10	US-10-257-017B-274757	Sequence 2
C 121	9.4	72.3	47.0	13	10	US-10-257-017B-25081	Sequence 2	C 194	8.4	70.0	42.0	12	10	US-10-257-017B-280041	Sequence 2
C 122	9.4	72.3	47.0	13	10	US-10-257-017B-25082	Sequence 2	C 195	8.4	70.0	42.0	12	10	US-10-257-017B-281085	Sequence 2
C 123	9.4	72.3	47.0	13	10	US-10-257-017B-27969	Sequence 2	C 196	8.4	70.0	42.0	12	10	US-10-257-017B-281930	Sequence 2
C 124	9.4	72.3	47.0	13	10	US-10-257-017B-27970	Sequence 2	C 197	8.4	70.0	42.0	12	10	US-10-257-017B-284490	Sequence 2
C 125	9.4	72.3	47.0	13	10	US-10-257-017B-36537	Sequence 3	C 198	8.4	70.0	42.0	12	10	US-10-257-017B-285659	Sequence 2
C 126	9.4	72.3	47.0	13	10	US-10-257-017B-36538	Sequence 3	C 199	8.4	70.0	42.0	12	10	US-10-257-017B-286867	Sequence 2
C 127	9.4	72.3	47.0	13	10	US-10-257-017B-56753	Sequence 5	C 200	8.4	70.0	42.0	12	10	US-10-257-017B-288407	Sequence 2
C 128	9.4	72.3	47.0	13	10	US-10-257-017B-56754	Sequence 5	C 201	8.4	70.0	42.0	12	10	US-10-257-017B-290224	Sequence 2
C 129	9.4	72.3	47.0	13	10	US-10-257-017B-96965	Sequence 9	C 202	8.4	70.0	42.0	12	10	US-10-257-017B-292655	Sequence 2
C 130	9.4	72.3	47.0	13	10	US-10-257-017B-96966	Sequence 9	C 203	8.4	70.0	42.0	12	10	US-10-257-017B-292658	Sequence 2
C 131	9.4	72.3	47.0	13	10	US-10-257-017B-111321	Sequence 1	C 204	8.4	70.0	42.0	12	10	US-10-257-017B-292707	Sequence 2
C 132	9.4	72.3	47.0	13	10	US-10-257-017B-111322	Sequence 1	C 205	8.4	70.0	42.0	12	10	US-10-257-017B-293121	Sequence 2
C 133	9.4	72.3	47.0	13	10	US-10-257-017B-117287	Sequence 1	C 206	8.4	70.0	42.0	12	10	US-10-257-017B-293477	Sequence 2
C 134	9.4	72.3	47.0	13	10	US-10-257-017B-117288	Sequence 1	C 207	8.4	70.0	42.0	12	10	US-10-257-017B-293667	Sequence 2
C 135	9.4	72.3	47.0	13	10	US-10-257-017B-117509	Sequence 1	C 208	8.4	70.0	42.0	12	10	US-10-257-017B-294586	Sequence 2
C 136	9.4	72.3	47.0	13	10	US-10-257-017B-117510	Sequence 1	C 209	8.4	70.0	42.0	12	10	US-10-257-017B-295090	Sequence 2
C 137	9.4	72.3	47.0	13	10	US-10-257-017B-187027	Sequence 1	C 210	8.4	70.0	42.0	12	10	US-10-257-017B-295284	Sequence 2
C 138	9.4	72.3	47.0	13	10	US-10-257-017B-187028	Sequence 1	C 211	8.4	70.0	42.0	12	10	US-10-257-017B-296295	Sequence 2
C 139	9.4	72.3	47.0	13	10	US-10-257-017B-215785	Sequence 2	C 212	8.4	70.0	42.0	12	10	US-10-257-017B-296487	Sequence 2
C 140	9.4	72.3	47.0	13	10	US-10-257-017B-215786	Sequence 2	C 213	8.4	70.0	42.0	12	10	US-10-257-017B-297323	Sequence 2
C 141	9.4	72.3	47.0	13	10	US-10-257-017B-235787	Sequence 2	C 214	8.4	70.0	42.0	12	10	US-10-257-017B-298042	Sequence 2
C 142	9.4	72.3	47.0	13	10	US-10-257-017B-235788	Sequence 2	C 215	8.4	70.0	42.0	12	10	US-10-257-017B-299239	Sequence 2
C 143	9.4	72.3	47.0	13	10	US-10-257-017B-248349	Sequence 2	C 216	8.4	70.0	42.0	12	10	US-10-257-017B-300438	Sequence 3
C 144	9.4	72.3	47.0	13	10	US-10-257-017B-248350	Sequence 2	C 217	8.4	70.0	42.0	12	10	US-10-257-017B-302312	Sequence 3
C 145	10	71.4	50.0	14	2	US-08-591-486B-34	Sequence 3	C 218	8.4	70.0	42.0	12	10	US-10-257-017B-302603	Sequence 3
C 146	10	71.4	50.0	14	11	US-10-984-919-858	Sequence 8	C 219	8.4	70.0	42.0	12	10	US-10-257-017B-302958	Sequence 3
C 147	12.8	70.1	64.0	18	12	US-10-310-914A-1258144	Sequence 1	C 220	8.4	70.0	42.0	12	10	US-10-257-017B-304877	Sequence 3
C 148	10.6	70.7	53.0	15	8	US-10-160-358-26	Sequence 2	C 221	8.4	70.0	42.0	12	10	US-10-257-017B-306204	Sequence 3
C 149	12	70.6	60.0	17	9	US-10-138-674-1646	Sequence 1	C 222	8.4	70.0	42.0	12	10	US-10-257-017B-306498	Sequence 3
C 150	12	70.6	60.0	17	9	US-10-138-674-1647	Sequence 1	C 223	8.4	70.0	42.0	12	10	US-10-257-017B-306928	Sequence 3
C 151	12	70.6	60.0	17	9	US-10-138-674-6253	Sequence 6	C 224	8.4	70.0	42.0	12	10	US-10-257-017B-309177	Sequence 3
C 152	12	70.6	60.0	17	9	US-10-138-674-6254	Sequence 6	C 225	8.4	70.0	42.0	12	10	US-10-257-017B-310209	Sequence 3
C 153	12	70.6	60.0	17	9	US-10-138-674-8571	Sequence 8	C 226	8.4	70.0	42.0	12	10	US-10-257-017B-310210	Sequence 3



Db 1 GCCCCAGTTGAAGTTGCCG 20

## RESULT 3

US-09-908-147-65  
; Sequence 65, Application US/09908147  
; Publication No. US20030144221A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/09/908,147  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 65  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-908-147-65

Query Match 90.0%; Score 18; DB 3; Length 20;  
Score over Length 90.0%;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCC 18  
Db 3 GCCCCAGTTGAAGTTGCC 20

## RESULT 4

US-10-728-509-65  
; Sequence 65, Application US/10728509  
; Publication No. US20040077583A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 65  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-728-509-65

Query Match 90.0%; Score 18; DB 9; Length 20;  
Score over Length 90.0%;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTTGCC 18  
Db 3 GCCCCAGTTGAAGTTGCC 20

## RESULT 5

US-09-908-147-5  
; Sequence 5, Application US/09908147  
; Publication No. US20030144221A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION

; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/09/908,147  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-09-908-147-5

Query Match 75.0%; Score 15; DB 3; Length 18;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTT 15  
Db 4 GCCCCAGTTGAAGTT 18

## RESULT 6

US-10-728-509-5  
; Sequence 5, Application US/10728509  
; Publication No. US20040077583A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-10-728-509-5

Query Match 75.0%; Score 15; DB 9; Length 18;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTGAAGTT 15  
Db 4 GCCCCAGTTGAAGTT 18

## RESULT 7

US-10-257-017B-271773/c  
; Sequence 271773, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 271773  
; LENGTH: 12  
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002613
US-10-257-017B-271773

Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1

RESULT 8
US-10-257-017B-274756/c
; Sequence 274756, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 274756
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003668
US-10-257-017B-274756

Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 10 AGTTGAAGTT 1

RESULT 9
US-10-257-017B-310208
; Sequence 310208, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310208
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023863
US-10-257-017B-310208
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Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16
Db 1 GTTGAAGTTG 10

RESULT 10
US-10-257-017B-341473/c
; Sequence 341473, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341473
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042053
US-10-257-017B-341473

Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 11 AGTTGAAGTT 2

RESULT 11
US-10-257-017B-353251
; Sequence 353251, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353251
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048401
US-10-257-017B-353251

Query Match      50.0%; Score 10; DB 10; Length 12;
Score over Length 83.3%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 6 AGTTGAAGTT 15  
|||||  
Db 1 AGTTGAAGTT 10

## RESULT 12

US-10-257-017B-355811/c  
; Sequence 355811, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/MO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 355811  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049826  
US-10-257-017B-355811

Query Match 50.0%; Score 10; DB 10; Length 12;  
Score over Length 83.3%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 10 AGTTGAAGTT 1

## RESULT 13

US-09-908-147-119  
; Sequence 119, Application US/09908147  
; Publication No. US20030144221A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/09/908,147  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 119  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-908-147-119

Query Match 82.0%; Score 16.4; DB 3; Length 20;  
Score over Length 82.0%;  
Best Local Similarity 94.4%; Pred. No. 6.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCCGT 20  
|||||  
Db 1 CCCAGTTGAAGTTGCCAT 18

## RESULT 14

US-10-728-509-119  
; Sequence 119, Application US/10728509  
; Publication No. US20040077593A1

; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 119  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-728-509-119

Query Match 82.0%; Score 16.4; DB 9; Length 20;  
Score over Length 82.0%;  
Best Local Similarity 94.4%; Pred. No. 6.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGTTGCCGT 20  
|||||  
Db 1 CCCAGTTGAAGTTGCCAT 18

## RESULT 15

US-08-591-486B-33  
; Sequence 33, Application US/08591486B  
; Publication No. US20020037866A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg F  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Göttingen, Wolfgang Brysch  
; TITLE OF INVENTION: A Pharmaceutical Composition  
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment  
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the  
; TITLE OF INVENTION: Treatment of Neoplasms  
; NUMBER OF SEQUENCES: 185  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/591,486B  
; FILING DATE: 11-JAN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93111059.7  
; FILING DATE: 10-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP94/02218  
; FILING DATE: 6-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William B.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10496/P60122  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 393-9350  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:



```
;
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-591-486B-33

Query Match          57.0%; Score 11.4; DB 2; Length 14;
Score over Length    81.4%;
Best Local Similarity 92.3%; Pred. No. 2.3e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
Db 2 GTTGAAGTTGCTG 14

RESULT 16
US-10-984-919-857
; Sequence 857, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 857
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-857

Query Match          57.0%; Score 11.4; DB 11; Length 14;
Score over Length    81.4%;
Best Local Similarity 92.3%; Pred. No. 2.3e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTGCCG 19
Db 2 GTTGAAGTTGCTG 14

RESULT 17
US-10-138-674-4126/c
; Sequence 4126, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4126

Query Match          60.0%; Score 12; DB 9; Length 15;
Score over Length    80.0%;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 18
US-10-287-949A-4126/c
; Sequence 4126, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4126

Query Match          60.0%; Score 12; DB 9; Length 15;
Score over Length    80.0%;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 19
US-10-951-303-4126/c
; Sequence 4126, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-4126

Query Match      60.0%; Score 12; DB 11; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 20
US-11-088-219-4126/c
; Sequence 4126, Application US/11088219
; Publication No. US20070042029A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: MCSwiggan, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Fact
; TITLE OF INVENTION: (VEGF-R)
; FILE REFERENCE: MBH800-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4126
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-4126

Query Match      60.0%; Score 12; DB 23; Length 15;
Score over Length 80.0%;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 21
US-10-257-017B-187031
; Sequence 187031, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187031
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187031

Query Match      52.0%; Score 10.4; DB 10; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 7.4e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
Db 1 AGTTGAAGTTGC 12

RESULT 22
US-10-257-017B-187032/c
; Sequence 187032, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187032
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187032

Query Match      52.0%; Score 10.4; DB 10; Length 13;
Score over Length 80.0%;
Best Local Similarity 91.7%; Pred. No. 7.4e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
Db 13 AGTTGAAGTTGC 2

RESULT 23
US-11-495-951A-94101
; Sequence 94101, Application US/11495951A
; Publication No. US20070111227A1
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAs AND METHODS OF USE
; FILE REFERENCE: 99689-00009
; CURRENT APPLICATION NUMBER: US/11/495,951A
; CURRENT FILING DATE: 2006-07-28
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
```

```
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 94101
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-495-951A-94101

Query Match      67.0%; Score 13.4; DB 27; Length 17;
Score over Length 78.8%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTGGCGT 20
   |||||
Db 3 AGTTGAAGTGGCGT 17
   |||||

RESULT 24
US-10-257-017B-275133/c
; Sequence 275133, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 275133
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003795
US-10-257-017B-275133

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
   |||||
Db 12 AGTTGAGTTG 2

RESULT 25
US-10-257-017B-280261
; Sequence 280261, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 280261
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010870
US-10-257-017B-280261
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008409
US-10-257-017B-280261

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
   |||||
Db 1 AGTTGAAGTTG 11
   |||||

RESULT 26
US-10-257-017B-281972/c
; Sequence 281972, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281972
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010216
US-10-257-017B-281972

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
   |||||
Db 11 AGTTGAGTTG 1

RESULT 27
US-10-257-017B-282569/c
; Sequence 282569, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 282569
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010870
US-10-257-017B-282569
```

```
Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
DB 12 AGTTGAGTTG 2

RESULT 28
US-10-257-017B-300630
; Sequence 300630, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300630
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019120
US-10-257-017B-300630

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
DB 2 AGTTGAGTTG 12

RESULT 29
US-10-257-017B-305246
; Sequence 305246, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 305246
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021354
US-10-257-017B-305246

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTTG 16
DB 2 AGTTGAGTTG 12

RESULT 30
US-10-257-017B-314348
; Sequence 314348, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314348
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026294
US-10-257-017B-314348

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
DB 2 AGTTAAAGTTG 12

RESULT 31
US-10-257-017B-329434
; Sequence 329434, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329434
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034943
US-10-257-017B-329434

Query Match      47.0%; Score 9.4; DB 10; Length 12;
Score over Length 78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
DB 1 AGTAGAAGTTG 11
```

```
RESULT 32
US-10-257-017B-337757
; Sequence 337757, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337757
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004732
US-10-257-017B-337757

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTAGAAGTTG 11

RESULT 33
US-10-257-017B-339358/c
; Sequence 339358, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 339358
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040958
US-10-257-017B-339358

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AATTGAAGTTG 11

RESULT 34
US-10-257-017B-345090/c
; Sequence 345090, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 345090
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043868
US-10-257-017B-345090

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTTGAAGTTG 11

RESULT 35
US-10-257-017B-361423
; Sequence 361423, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 361423
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052630
US-10-257-017B-361423

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTTGAAGTTG 11

RESULT 36
US-10-257-017B-28743
; Sequence 28743, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 28743
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004732
US-10-257-017B-28743

Query Match          47.0%; Score 9.4; DB 10; Length 12;
Score over Length    78.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AATTGAAGTTG 11
```

; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 28743  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008356  
US-10-257-017B-28743

Query Match 50.0%; Score 10; DB 10; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
|||||  
Db 1 AGTTGAAGTT 10  
|||||

## RESULT 37

US-10-257-017B-28744/c  
; Sequence 28744, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 28744  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008356  
US-10-257-017B-28744

Query Match 50.0%; Score 10; DB 10; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
|||||  
Db 13 AGTTGAAGTT 4  
|||||

## RESULT 38

US-10-257-017B-65609  
; Sequence 65609, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 65609  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017271  
US-10-257-017B-65609

Query Match 50.0%; Score 10; DB 10; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
|||||  
Db 4 AGTTGAAGTT 13  
|||||

## RESULT 39

US-10-257-017B-65610/c  
; Sequence 65610, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 65610  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017271  
US-10-257-017B-65610

Query Match 50.0%; Score 10; DB 10; Length 13;  
Score over Length 76.9%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
|||||  
Db 10 AGTTGAAGTT 1  
|||||

## RESULT 40

US-10-257-017B-107775  
; Sequence 107775, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 107775  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026982
US-10-257-017B-107775

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
DB      3 AGTTGAAGTT 12

RESULT 41
US-10-257-017B-107776/c
; Sequence 107776, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 107776
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026982
US-10-257-017B-107776

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
DB      11 AGTTGAAGTT 2

RESULT 42
US-10-257-017B-131257
; Sequence 131257, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131257
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032754
US-10-257-017B-131257

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
DB      11 AGTTGAAGTT 2
```

```
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
DB      1 GTTGAAGTTG 10

RESULT 43
US-10-257-017B-131258/c
; Sequence 131258, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131258
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032754
US-10-257-017B-131258

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
DB      13 GTTGAAGTTG 4

RESULT 44
US-10-257-017B-150111
; Sequence 150111, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 150111
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037893
US-10-257-017B-150111

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
```

```
Db          |||||
            4 AGTTGAAGTT 13

RESULT 45
US-10-257-017B-150112/c
; Sequence 150112, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 150112
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037893
US-10-257-017B-150112

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 AGTTGAAGTT 15
            |||||
            10 AGTTGAAGTT 1

RESULT 46
US-10-257-017B-153411
; Sequence 153411, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 153411
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038780
US-10-257-017B-153411

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          6 AGTTGAAGTTGC 17
            |||||
            2 AGTTGAAGTTG 13

RESULT 47
US-10-257-017B-153412/c
; Sequence 153412, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 153412
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038780
US-10-257-017B-153412

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          6 AGTTGAAGTTGC 17
            |||||
            12 AGTTGAAGATGY 1

RESULT 48
US-10-257-017B-171651
; Sequence 171651, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171651
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042787
US-10-257-017B-171651

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 AGTTGAAGTT 15
            |||||
            2 AGTTGAAGTT 11

RESULT 49
US-10-257-017B-171652/c
; Sequence 171652, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```



```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171652
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042787
US-10-257-017B-171652

Query Match      50.0%; Score 10; DB 10; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
      |||||
Db      12 AGTTGAAGTT 3

RESULT 50
US-11-051-720-809
; Sequence 809, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 809
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-051-720-809

Query Match      50.0%; Score 10; DB 21; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
      |||||
Db      3 GTTGAAGTTG 12

RESULT 51
US-11-043-842-704
; Sequence 704, Application US/11043842
; Publication No. US20060183131A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 1847.1004
; CURRENT APPLICATION NUMBER: US/11/043,842
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1028
; SEQ ID NO 704
; LENGTH: 13
; TYPE: DNA
```

```
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-043-842-704

Query Match      50.0%; Score 10; DB 22; Length 13;
Score over Length 76.9%;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
      |||||
Db      3 GTTGAAGTTG 12

RESULT 52
US-10-535-164-454911/c
; Sequence 454911, Application US/10535164
; Publication No. US20070134655A1
; GENERAL INFORMATION:
; APPLICANT: BENTWICH, ITZHAK
; TITLE OF INVENTION: Bioinformatically detectable of Novel Regulatory genes and thereof
; FILE REFERENCE: 050992.0200.PCUS13
; CURRENT APPLICATION NUMBER: US/10/535,164
; CURRENT FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 548156
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 454911
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Human
; OTHER INFORMATION:
US-10-535-164-454911

Query Match      64.0%; Score 12.8; DB 17; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 4.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 CCCAGTTGAAGTTGCC 18
      |||||
Db      16 CCCAGGTGAAGGTGCC 1

RESULT 53
US-11-495-951A-101428/c
; Sequence 101428, Application US/11495951A
; Publication No. US2007011227A1
; GENERAL INFORMATION:
; APPLICANT: GREEN, PAMELA
; APPLICANT: MEYERS, BLAKE
; APPLICANT: LU, CHENG
; APPLICANT: TEJ, SHIVAKUNDAN SINGH
; APPLICANT: SOURET, FREDERIC
; TITLE OF INVENTION: SMALL REGULATORY RNAs AND METHODS OF USE
; FILE REFERENCE: 99689-00009
; CURRENT APPLICATION NUMBER: US/11/495,951A
; CURRENT FILING DATE: 2006-07-28
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/772,666
; PRIOR FILING DATE: 2006-02-13
; PRIOR APPLICATION NUMBER: 60/703,215
; PRIOR FILING DATE: 2005-07-28
; NUMBER OF SEQ ID NOS: 185413
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101428
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-495-951A-101428

Query Match      64.0%; Score 12.8; DB 27; Length 17;
Score over Length 75.3%;
Best Local Similarity 87.5%; Pred. No. 4.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 2 CCCAGTTGAAGTTGC 17  
||||| |||||||  
Db 16 CCCAGGGAAGTTGC 1

## RESULT 54

US-10-257-017B-272526  
; Sequence 272526, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 272526  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonukleotid-Primer  
US-10-257-017B-272526

Query Match 45.0%; Score 9; DB 10; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14  
|||||  
Db 4 AGTTGAAGT 12

## RESULT 55

US-10-257-017B-281370/c  
; Sequence 281370, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 281370  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009690  
US-10-257-017B-281370

Query Match 45.0%; Score 9; DB 10; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15  
|||||  
Db 11 GTTGAAGTT 3

## RESULT 56

US-10-257-017B-284630/c  
; Sequence 284630, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 284630  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011911  
US-10-257-017B-284630

Query Match 45.0%; Score 9; DB 10; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14  
|||||  
Db 12 AGTTGAAGT 4

## RESULT 57

US-10-257-017B-288152  
; Sequence 288152, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 288152  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013396  
US-10-257-017B-288152

Query Match 45.0%; Score 9; DB 10; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16  
|||||  
Db 2 TTGAAGTTG 10

## RESULT 58

US-10-257-017B-298602  
; Sequence 298602, Application US/10257017B  
; Publication No. US20040241651A1

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 298602
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018187
US-10-257-017B-298602

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGAAGTTGC 17
Db 4 TGAAGTTGC 12

RESULT 59
US-10-257-017B-298745
; Sequence 298745, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 298745
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide-Primer
US-10-257-017B-298745

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GTTGAAGTT 15
Db 4 GTTGAAGTT 12

RESULT 60
US-10-257-017B-299931
; Sequence 299931, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299931
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018813
US-10-257-017B-299931

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTGAAGTTG 16
Db 2 TTGAAGTTG 10

RESULT 61
US-10-257-017B-303341/c
; Sequence 303341, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303341
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020445
US-10-257-017B-303341

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGTTGAAGT 14
Db 11 AGTTGAAGT 3

RESULT 62
US-10-257-017B-305026
; Sequence 305026, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 305026  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021217  
US-10-257-017B-305026

Query Match 45.0%; Score 9; DB 10; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15  
DB 4 GTTGAAGTT 12

RESULT 63  
US-10-257-017B-307994  
; Sequence 307994, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 307994  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022828  
US-10-257-017B-307994

Query Match 45.0%; Score 9; DB 10; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15  
DB 4 GTTGAAGTT 12

RESULT 64  
US-10-257-017B-310012  
; Sequence 310012, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 310012  
; LENGTH: 12  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023776  
US-10-257-017B-310012

Query Match 45.0%; Score 9; DB 10; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16  
DB 2 TTGAAGTTG 10

RESULT 65  
US-10-257-017B-319646/c  
; Sequence 319646, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 319646  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029341  
US-10-257-017B-319646

Query Match 45.0%; Score 9; DB 10; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16  
DB 12 TTGAAGTTG 4

RESULT 66  
US-10-257-017B-332564/c  
; Sequence 332564, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 332564  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036994  
US-10-257-017B-332564

```
Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
DB 12 TTGAAGTTG 4

RESULT 67
US-10-257-017B-333972
; Sequence 333972, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 333972
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037861
US-10-257-017B-333972

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
DB 2 TTGAAGTTG 10

RESULT 68
US-10-257-017B-337673
; Sequence 337673, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337673
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039994
US-10-257-017B-337673

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
DB 2 TTGAAGTTG 10

RESULT 69
US-10-257-017B-338530/c
; Sequence 338530, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338530
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005251
US-10-257-017B-338530

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTG 16
DB 12 TTGAAGTTG 4

RESULT 70
US-10-257-017B-338626/c
; Sequence 338626, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338626
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040587
US-10-257-017B-338626

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTT 15
DB 9 GTTGAAGTT 1
```

```
RESULT 71
US-10-257-017B-342781
; Sequence 342781, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 342781
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042707
US-10-257-017B-342781

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 8 TTGAAGTTG 16
Db 1 TTGAAGTTG 9

RESULT 72
US-10-257-017B-343923/c
; Sequence 343923, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 343923
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043299
US-10-257-017B-343923

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 7 GTTGAAGTT 15
Db 10 GTTGAAGTT 2

RESULT 73
US-10-257-017B-345821/c
; Sequence 345821, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 345821
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044228
US-10-257-017B-345821

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 7 GTTGAAGTT 15
Db 9 GTTGAAGTT 1

RESULT 74
US-10-257-017B-358109
; Sequence 358109, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358109
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050957
US-10-257-017B-358109

Query Match 45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 8 TTGAAGTTG 16
Db 1 TTGAAGTTG 9

RESULT 75
US-10-257-017B-360215/c
; Sequence 360215, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 360215
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050957
US-10-257-017B-360215/c
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 360215
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051979
US-10-257-017B-360215

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGTTGAAGT 14
DB      10 AGTTGAAGT 2

RESULT 76
US-10-257-017B-365894/c
; Sequence 365894, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 365894
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0055428
US-10-257-017B-365894

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TTGAAGTTG 16
DB      12 TTGAAGTTG 4

RESULT 77
US-10-257-017B-369254
; Sequence 369254, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369254
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057554
US-10-257-017B-369254

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTTGAAGTT 15
DB      4 GTTGAAGTT 12

RESULT 78
US-10-257-017B-369635/c
; Sequence 369635, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369635
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057764
US-10-257-017B-369635

Query Match      45.0%; Score 9; DB 10; Length 12;
Score over Length 75.0%;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TTGAAGTTG 16
DB      9 TTGAAGTTG 1

RESULT 79
US-10-257-017B-379943
; Sequence 379943, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379943
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

;  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063547  
US-10-257-017B-379943

Query Match 45.0%; Score 9; DB 10; Length 12;  
Score over Length 75.0%;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGTTGAAGT 14  
||| |||||  
DB 4 AGTTGAAGT 12

## RESULT 80

US-09-168-791-14/c

; Sequence 14, Application US/09168791

; Publication No. US20030100519A1

; GENERAL INFORMATION:

; APPLICANT: Richelson, Elliott

; APPLICANT: Tyler, Beth Marie

; APPLICANT: Cusack, Bernadette Marie

; APPLICANT: Douglas, Christopher Lee

; APPLICANT: Jansen, Karen

; TITLE OF INVENTION: USING POLYAMIDE NUCLEIC ACID OLIGOMERS

; FILE REFERENCE: 07039/126001

; CURRENT APPLICATION NUMBER: US/09/168,791

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 14

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Rat

US-09-168-791-14

Query Match 52.0%; Score 10.4; DB 3; Length 14;  
Score over Length 74.3%;  
Best Local Similarity 91.7%; Pred. No. 7.4e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16  
||| |||||  
DB 14 CAGATGAAGTTG 3

## RESULT 81

US-10-799-238-14/c

; Sequence 14, Application US/10799238

; Publication No. US2004022489A1

; GENERAL INFORMATION:

; APPLICANT: Richelson, Elliott

; APPLICANT: Tyler, Beth Marie

; APPLICANT: Cusack, Bernadette Marie

; APPLICANT: Douglas, Christopher Lee

; APPLICANT: Jansen, Karen

; TITLE OF INVENTION: USING POLYAMIDE NUCLEIC ACID OLIGOMERS

; FILE REFERENCE: 07039/126001

; CURRENT APPLICATION NUMBER: US/10/799,238

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 14

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Rat

US-10-799-238-14

Query Match 52.0%; Score 10.4; DB 10; Length 14;

Score over Length 74.3%;  
Best Local Similarity 91.7%; Pred. No. 7.4e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16  
||| |||||  
DB 14 CAGATGAAGTTG 3

## RESULT 82

US-10-257-017B-61663

; Sequence 61663, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; PRIOR FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 61663

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016401

US-10-257-017B-61663

Query Match 48.0%; Score 9.6; DB 10; Length 13;  
Score over Length 73.8%;  
Best Local Similarity 90.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTGC 17  
||| |||||  
DB 4 TTGAAGTTGY 13

## RESULT 83

US-10-257-017B-61664/c

; Sequence 61664, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; PRIOR FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 61664

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016401

US-10-257-017B-61664

Query Match 48.0%; Score 9.6; DB 10; Length 13;  
Score over Length 73.8%;  
Best Local Similarity 90.0%; Pred. No. 1.9e+06;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGAAGTTGC 17



```
Db          10 TTGAAGTTGY 1
|||||
RESULT 84
US-10-138-674-5807
; Sequence 5807, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5807

Query Match          59.0%; Score 11.8; DB 9; Length 16;
Score over Length    73.8%;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
   |||||:||||:
Db 2 GACCCAGAUGAAGUU 16

RESULT 85
US-10-287-949A-5807
; Sequence 5807, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5807

Query Match          59.0%; Score 11.8; DB 9; Length 16;
Score over Length    73.8%;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
   |||||:||||:
Db 2 GACCCAGAUGAAGUU 16

RESULT 86
US-11-088-219-5807
; Sequence 5807, Application US/11088219
```

```
; Publication No. US20070042029A1
; GENERAL INFORMATION:
; APPLICANT: Sinna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor
; FILE REFERENCE: MBH00-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5807
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-5807

Query Match          59.0%; Score 11.8; DB 23; Length 16;
Score over Length    73.8%;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTT 15
   |||||:||||:
Db 2 GACCCAGAUGAAGUU 16

RESULT 87
US-10-714-333A-764639/c
; Sequence 764639, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 764639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-764639

Query Match          70.0%; Score 14; DB 15; Length 19;
Score over Length    73.7%;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 7 GTTGAAGTTGCCGT 20  
Db 16 GTTGAAGTTGCCGT 3

## RESULT 88

US-11-083-784-764639/c  
; Sequence 764639, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-764639

Query Match 70.0%; Score 14; DB 19; Length 19;  
Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20  
Db 16 GTTGAAGTTGCCGT 3

## RESULT 89

US-11-101-244-764639/c  
; Sequence 764639, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 764639  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-764639

Query Match 70.0%; Score 14; DB 20; Length 19;

Score over Length 73.7%;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTGCCGT 20  
Db 16 GTTGAAGTTGCCGT 3

## RESULT 90

US-09-504-231A-1284/c  
; Sequence 1284, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED  
; FILE REFERENCE: IPI 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1284  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-1284

Query Match 55.0%; Score 11; DB 3; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAG 13  
Db 15 CCCAGTTGAAG 5

## RESULT 91

US-09-274-553D-1284/c  
; Sequence 1284, Application US/09274553D  
; Patent No. US20020082225A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED  
; FILE REFERENCE: IPI 247/282  
; CURRENT APPLICATION NUMBER: US/09/274,553D  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27

Query Match 55.0%; Score 11; DB 3; Length 15;

4 CCAGTTGAAGT 14

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Db          15 CCAGTTGAAGT 5
|||||
RESULT 94

```

US-10-931-303-4130/C  
; Sequence 4150, Application US/10951303  
; Publication No. US20050227937A1  
; GENERAL INFORMATION:

APPLICANT: McSwiggen, Jim  
 APPLICANT: Stinchcomb, Dan  
 APPLICANT: Escobedo, Jaime  
 TITLE OF INVENTION: Method and Reagent for Treatment of Dis-  
 ease of Vascular Endothelial Growth  
 FILE REFERENCE: MEH00-876-K (400/021)  
 CURRENT APPLICATION NUMBER: US/10/951,303  
 CURRENT FILING DATE: 2004-09-27  
 PRIOR APPLICATION NUMBER: US/09/685,664  
 PRIOR FILING DATE: 2000-10-10  
 PRIOR APPLICATION NUMBER: US 60/005,974  
 PRIOR FILING DATE: 1995-10-26  
 PRIOR APPLICATION NUMBER: US 08/584,040  
 PRIOR FILING DATE: 1996-01-08  
 PRIOR APPLICATION NUMBER: US 09/371,772  
 PRIOR FILING DATE: 1999-08-10  
 NUMBER OF SEQ ID NOS: 8231  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 4150  
 LENGTH: 15  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-10-951-303-4150

Query Match 55.0%; Score 11; DB 11; Length 15  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels

		MALINES	11; CONSERVATIVE	V, MISMATCHES V, INDEL
Qy	4	CCAGTTGAAGT	14	
D6	15	CCAGTTGAAGT	5	

RESULT 95  
US-11-088-219-4150/c  
; Sequence 4150, Application US/11088219  
; Publication No. US20070042029A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment  
; TITLE OF INVENTION: Conditions Related to Levels of Vascular  
; TITLE OF INVENTION: (VEGF-R)  
; FILE REFERENCE: MBHB00-876-Q (400/266)  
; CURRENT APPLICATION NUMBER: US/11/088,219  
; CURRENT FILING DATE: 2005-03-23  
; PRIOR APPLICATION NUMBER: 10/138,674  
; PRIOR FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: 09/870,161  
; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: 09/708,690  
; PRIOR FILING DATE: 2000-11-07  
; CURRENT APPLICATION NUMBER: 09/371,722  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 08/584,040  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4150  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-088-219-4150

Query Match 55.0%; Score 11; DB 23; Length 15;  
Score over Length 73.3%;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
|||||  
DB 15 CCAGTTGAAGT 5

RESULT 96  
US-10-477-086-15  
; Sequence 15, Application US/10477086  
; Publication No. US2004023497A1  
; GENERAL INFORMATION:  
; APPLICANT: GONG, Da-Wei  
; APPLICANT: SCHULDINER, Alan  
; APPLICANT: YANG, Rongze  
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE  
; FILE REFERENCE: UMB-01-032  
; CURRENT APPLICATION NUMBER: US/10/477,086  
; PRIOR FILING DATE: 2003-11-06  
; PRIOR APPLICATION NUMBER: US 60/290,829  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: PCT/US02/15103  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: 3'clip  
; LOCATION: (1)..(12)  
; OTHER INFORMATION: ALT2 Exon 3, intron/exon junction, 3' splice acceptor  
US-10-477-086-15

Query Match 44.0%; Score 8.8; DB 10; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 4.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCAGTTGAAG 13  
|||||  
DB 1 CCCAGTTGAAGT 12

RESULT 97  
US-10-257-017B-275104/c  
; Sequence 275104, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 275104  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003785  
US-10-257-017B-275104

Query Match 44.0%; Score 8.8; DB 10; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 4.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAA 12  
|||||  
DB 12 GCCCCACTTTAA 1

RESULT 98  
US-10-257-017B-290891  
; Sequence 290891, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 290891  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014559  
US-10-257-017B-290891

Query Match 44.0%; Score 8.8; DB 10; Length 12;  
Score over Length 73.3%;  
Best Local Similarity 83.3%; Pred. No. 4.8e+06;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17  
|||||  
DB 1 AGTTGATGTAGC 12

RESULT 99  
US-10-257-017B-317181/c  
; Sequence 317181, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317181
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027856
US-10-257-017B-317181

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 TTGAAGTTGCCG 19
Db      12 TTGGAGTTGGCG 1

RESULT 100
US-10-257-017B-322885
; Sequence 322885, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322885
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031095
US-10-257-017B-322885

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTGC 17
Db      1 AGTAGAAGTGC 12

RESULT 101
US-10-257-017B-323132/c
; Sequence 323132, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323132
; LENGTH: 12
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031232
US-10-257-017B-323132

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCCCAGTTGAA 12
Db      12 GCGCAGTTGAA 1

RESULT 102
US-10-257-017B-326883
; Sequence 326883, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 326883
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033322
US-10-257-017B-326883

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 TGAAGTTGCCGT 20
Db      1 TGAGGTTGCGT 12

RESULT 103
US-10-257-017B-327149/c
; Sequence 327149, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 327149
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033464
US-10-257-017B-327149
```

```
Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 12 TGAAGTTGGGT 1

RESULT 104
US-10-257-017B-344782
; Sequence 344782, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 344782
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043703
US-10-257-017B-344782

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
DB 1 AGTTGAGATTGC 12

RESULT 105
US-10-257-017B-353467
; Sequence 353467, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353467
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048527
US-10-257-017B-353467

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 9 TGAAGTTGCCGT 20
DB 1 TGAAGTGGACGT 12

RESULT 106
US-10-257-017B-358049/C
; Sequence 358049, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358049
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050929
US-10-257-017B-358049

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCGT 20
DB 12 TGAAGTTGGAGT 1

RESULT 107
US-10-257-017B-369872
; Sequence 369872, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369872
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057857
US-10-257-017B-369872

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
DB 1 AGTTGGAGTTTC 12
```

```
RESULT 108
US-10-257-017B-373811
; Sequence 373811, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 373811
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060333
US-10-257-017B-373811

Query Match      44.0%; Score 8.8; DB 10; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGC 17
Db 1 AGTTGATTTGC 12

RESULT 109
US-10-591-442-27/c
; Sequence 27, Application US/10591442
; Publication No. US20070161001A1
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-27

Query Match      44.0%; Score 8.8; DB 17; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1

RESULT 110
US-10-591-442-29/c
; Sequence 29, Application US/10591442
; Publication No. US20070161001A1
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; TITLE OF INVENTION: EXPRESSION
```

```
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-29

Query Match      44.0%; Score 8.8; DB 17; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGCTGAAGCTG 1

RESULT 111
US-10-591-442-45/c
; Sequence 45, Application US/10591442
; Publication No. US20070161001A1
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: QUANTIFYING AND PROFILING ANTIBODY AND T CELL RECEPTOR GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 32488
; CURRENT APPLICATION NUMBER: US/10/591,442
; CURRENT FILING DATE: 2006-09-01
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-591-442-45

Query Match      44.0%; Score 8.8; DB 17; Length 12;
Score over Length 73.3%;
Best Local Similarity 83.3%; Pred. No. 4.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTG 16
Db 12 CAGTTGAACCTG 1

RESULT 112
US-11-126-421-15
; Sequence 15, Application US/11126421
; Publication No. US20050214883A1
; GENERAL INFORMATION:
; APPLICANT: GONG, Da-Wei
; APPLICANT: SCHULDNER, Alan
; APPLICANT: YANG, Rongze
; TITLE OF INVENTION: NOVEL ALANINE TRANSAMINASE ENZYME AND METHODS OF USE
; FILE REFERENCE: UMB-01-032
; CURRENT APPLICATION NUMBER: US/11/126,421
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/10/477,086
; PRIOR FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 60/290,829
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: PCT/US02/15103
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 37
```

```

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 3'clip
; LOCATION: (1)..(12)
; OTHER INFORMATION: ALT2 Exon
US..11-126-421..15

```

Query Match	44.0%	Score 8.8;	DB 18;	Length 12;
Score over Length	73.3%			
Best Local Similarity	83.3%	Pred. No. 4.8e+06;		
Matches 10; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 2 CCCAGTTGAAG 13  
| | | | | | | |  
Db 1 CCCAGGTGATG 12

```

RESULT 113
US-11-585-939A-7/c
; Sequence 7, Application US/11585939A
; Publication No. US20070138013A1
; GENERAL INFORMATION:
; APPLICANT: HAYASHI, Miho
; APPLICANT: MORI, Kazuyoshi
; APPLICANT: MAEDA, Mizuo
; TITLE OF INVENTION: DNA SEPARATION DEVICE, AND LIGAND DNA
; FILE REFERENCE: 2006.1856A
; CURRENT APPLICATION NUMBER: US/11/585,939A
; CURRENT FILING DATE: 2006-10-25
; PRIOR APPLICATION NUMBER: JP 2005-311933
; PRIOR FILING DATE: 2005-10-26
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-585-939A-7

```

Query Match	44.0%	Score 8.8;	DB 27;	Length 12;
Score over Length	73.3%			
Best Local Similarity	83.3%	Pred. No. 4.8e+05;		
Matches 10: Conservative		0: Mismatches 2;	Indels 0;	Gaps 0;

QY 2 CCCAGTTGAAG 13  
12 CCCCCCCCCC  
db 12 CCCAGCCGAAG 1

```

RESULT 114
US-10-310-914A-801404/c
; Sequence 801404, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruszat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 801404
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-801404

```

Query Match 69.0%; Score 13.8; DB 12; Length 19;

```
Score over Length      72.6%;
Best Local Similarity  88.2%;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 CCCAGTTGAAGTTGCC 18  
Db 17 CCACATTTGAAGTTGCC 1

```

RESULT 115
US-10-257-017B-6223
; Sequence 6223, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 6223
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001948
US-10-257-017B-6223

```

Query Match 47.0%; Score 9.4; DB 10; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 2.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
||| |||||  
Db 3 AGTAGAAGTTG 13

```

RESULT 116
US-10-257-017B-6224/c
; Sequence 6224, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 6224
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001948
US-10-257-017B-6224

```

```

Query Match          47.0%;      Score 9.4;  DB 10;  Length 13;
Score over Length   72.3%;
Best Local Similarity 90.9%;      Pred. No. 2.4e+06;
Matches 10;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

QY 6 AGTTGAAGTTG 16



```
Db      11  ACTGAAGTTG 1
|||||
RESULT 117
US-10-257-017B-12629
; Sequence 12629, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12629
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002968
US-10-257-017B-12629
Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  AGTTGAAGTTG 16
|||||
Db      2  AGTTGATGTTG 12
|||||
RESULT 118
US-10-257-017B-12630/c
; Sequence 12630, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12630
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002968
US-10-257-017B-12630
Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  AGTTGAAGTTG 16
|||||
Db      12 AGTTGATGTTG 2
|||||
RESULT 119
US-10-257-017B-12630/c
; Sequence 12630, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12630
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25055
Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9  TGAAGTTGCGC 19
|||||
Db      3  TGAAGTTGTCG 13
|||||
RESULT 120
US-10-257-017B-25056/c
; Sequence 25056, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25056
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006071
US-10-257-017B-25056
Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9  TGAAGTTGCGC 19
|||||
Db      11 TGAAGTTGTCG 1
|||||
RESULT 121
US-10-257-017B-25081
; Sequence 25081, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25081
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006096
US-10-257-017B-25081

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
      ||| ||| ||| |||
Db      2 AGTGGAAGTTG 12

RESULT 122
US-10-257-017B-25082/c
; Sequence 25082, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 25082
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006096
US-10-257-017B-25082

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
      ||| ||| ||| |||
Db      12 AGTGGAAGTTG 2

RESULT 123
US-10-257-017B-27969
; Sequence 27969, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 27969
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007879
US-10-257-017B-27969

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
      ||| ||| ||| |||
Db      1 AGTTGAAGTTG 11

RESULT 124
US-10-257-017B-27970/c
; Sequence 27970, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 27970
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007879
US-10-257-017B-27970

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
      ||| ||| ||| |||
Db      13 AGTTGAAGTTG 3

RESULT 125
US-10-257-017B-36537
; Sequence 36537, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 36537
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011456
US-10-257-017B-36537

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 ATTGAAGTTG 11

RESULT 126
US-10-257-017B-36538/c
; Sequence 36538, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 36538
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011456
US-10-257-017B-36538

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 ATTGAAGTTG 3

RESULT 127
US-10-257-017B-56753
; Sequence 56753, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 56753
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56753

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      1 AGTTGAATTTG 11

RESULT 128
US-10-257-017B-56754/c
; Sequence 56754, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 56754
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015377
US-10-257-017B-56754

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTTG 16
Db      13 AGTTGAATTTG 3

RESULT 129
US-10-257-017B-96965
; Sequence 96965, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96965
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054
US-10-257-017B-96965

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
```

```
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
   |||||
Db 1 TGAAGTTGCCG 11

RESULT 130
US-10-257-017B-96966/c
; Sequence 96966, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96966
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054
US-10-257-017B-96966

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
   |||||
Db 13 TGAAGTTGCCG 3

RESULT 131
US-10-257-017B-111321
; Sequence 111321, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111321
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809
US-10-257-017B-111321

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   |||||
Db 3 AGTTGAAGTTG 13

RESULT 132
US-10-257-017B-111322/c
; Sequence 111322, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111322
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809
US-10-257-017B-111322

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   |||||
Db 11 AGTTGAAGTTG 1

RESULT 133
US-10-257-017B-117287
; Sequence 117287, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117287
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029345
US-10-257-017B-117287

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   |||||
Db 3 AGTTGAAGTTG 13

RESULT 134
US-10-257-017B-117288/c
```

```
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
   |||||
Db 1 TGAAGTTGCCG 11

RESULT 130
US-10-257-017B-96966/c
; Sequence 96966, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 96966
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024054
US-10-257-017B-96966

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGAAGTTGCCG 19
   |||||
Db 13 TGAAGTTGCCG 3

RESULT 131
US-10-257-017B-111321
; Sequence 111321, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111321
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809
US-10-257-017B-111321

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   |||||
Db 3 AGTTGAAGTTG 13

RESULT 132
US-10-257-017B-111322/c
; Sequence 111322, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111322
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027809
US-10-257-017B-111322

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   |||||
Db 11 AGTTGAAGTTG 1

RESULT 133
US-10-257-017B-117287
; Sequence 117287, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117287
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029345
US-10-257-017B-117287

Query Match 47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16
   |||||
Db 3 AGTTGAAGTTG 13

RESULT 134
US-10-257-017B-117288/c
```

; Sequence 117288, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations

; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 117288

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029345

US-10-257-017B-117288

Query Match 47.0%; Score 9.4; DB 10; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 2.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 11 AGTTGAGTTG 1

RESULT 135

US-10-257-017B-117509

; Sequence 117509, Application US/10257017B  
; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 117509

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029385

US-10-257-017B-117509

Query Match 47.0%; Score 9.4; DB 10; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 2.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 3 AGTTGAAGTTG 13

RESULT 136

US-10-257-017B-117510/c

; Sequence 117510, Application US/10257017B  
; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 117510

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029385

US-10-257-017B-117510

Query Match 47.0%; Score 9.4; DB 10; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 2.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 11 AGTTGAAGTTG 1

RESULT 137

US-10-257-017B-187027

; Sequence 187027, Application US/10257017B  
; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 187027

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102

US-10-257-017B-187027

Query Match 47.0%; Score 9.4; DB 10; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 2.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
Db 1 AGTTGAAGTTG 11

RESULT 138

US-10-257-017B-187028/c

; Sequence 187028, Application US/10257017B  
; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

```
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187028
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046102
US-10-257-017B-187028

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 13 AGTTGAAGTTG 3

RESULT 139
US-10-257-017B-215785
; Sequence 215785, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 215785
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052481
US-10-257-017B-215785

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 13 AGTTGAAGTTG 3

RESULT 140
US-10-257-017B-215786/c
; Sequence 215786, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 215786
```

```
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052481
US-10-257-017B-215786

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 13 AGTTGAAGTTG 3

RESULT 141
US-10-257-017B-235787
; Sequence 235787, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 235787
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
US-10-257-017B-235787

Query Match      47.0%; Score 9.4; DB 10; Length 13;
Score over Length 72.3%;
Best Local Similarity 90.9%; Pred. No. 2.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTTG 16
Db 13 AGTTGAAGTTG 11

RESULT 142
US-10-257-017B-235788/c
; Sequence 235788, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 235788
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009202
```

## US-10-257-017B-235788

Query Match 47.0%; Score 9.4; DB 10; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 2.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
DB 13 AGTGGAGTTG 3

## RESULT 143

US-10-257-017B-248349  
; Sequence 248349, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 248349  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0060684  
US-10-257-017B-248349

Query Match 47.0%; Score 9.4; DB 10; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 2.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTG 16  
|||||  
DB 1 AGTTGAGTTG 11

## RESULT 144

US-10-257-017B-248350/c  
; Sequence 248350, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 248350  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0060684  
US-10-257-017B-248350

Query Match 47.0%; Score 9.4; DB 10; Length 13;  
Score over Length 72.3%;  
Best Local Similarity 90.9%; Pred. No. 2.4e+06;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 AGTTGAAGTTG 16  
|||||  
DB 13 AGTTGAGTTG 3

## RESULT 145

US-08-591-486B-34  
; Sequence 34, Application US/08591486B  
; Publication No. US20020037866A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg F  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Göttingen, Wolfgang Brysch  
; TITLE OF INVENTION: A Pharmaceutical Composition  
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment  
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the  
; TITLE OF INVENTION: Treatment of Neoplasms  
; NUMBER OF SEQUENCES: 185  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/591,486B  
; FILING DATE: 11-JAN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93111059.7  
; FILING DATE: 10-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP94/02218  
; FILING DATE: 6-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10496/P60122  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 393-9350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; TOPOLOGY: unknown  
; STRANDEDNESS: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-08-591-486B-34

Query Match 50.0%; Score 10; DB 2; Length 14;  
Score over Length 71.4%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
|||||  
DB 5 GTTGAAGTTG 14

RESULT 146  
US-10-984-919-858  
; Sequence 858, Application US/10984919

; Publication No. US20050130927A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlengersien, Karl-Hermann  
; APPLICANT: Brysch, Wolfgang  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
; FILE REFERENCE: 10496/P63763USO  
; CURRENT APPLICATION NUMBER: US/10/984,919  
; PRIOR FILING DATE: 2004-11-10  
; PRIOR APPLICATION NUMBER: US/09/341,700  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: PCT/EP98/00497  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: EP 97 101 531.8  
; PRIOR FILING DATE: 1997-01-31  
; NUMBER OF SEQ ID NOS: 1764  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 858  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: antisense oligonucleotide  
US-10-984-919-858

Query Match 50.0%; Score 10; DB 11; Length 14;  
Score over Length 71.4%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
DB 5 GTTGAAGTTG 14  
|||||

RESULT 147  
US-10-310-914A-1258144/c  
; Sequence 1258144, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1258144  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1258144

Query Match 64.0%; Score 12.8; DB 12; Length 18;  
Score over Length 71.1%;  
Best Local Similarity 87.5%; Pred. No. 4.5e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CAGTTGAAGTTGCCGT 20  
DB 17 CAGTTGAAGTGCAGT 2  
|||||

RESULT 148  
US-10-160-358-26  
; Sequence 26, Application US/10160358  
; Publication No. US20030198969A1  
; GENERAL INFORMATION:  
; APPLICANT: Genesance Pharmaceuticals, Inc.  
; APPLICANT: Blegiecki, Karyn  
; APPLICANT: Cappola, Gina-Marie

; APPLICANT: Koshiy, Beena  
; APPLICANT: Monroe, Glen  
; TITLE OF INVENTION: HAPLOTYPES OF THE TACR2 GENE  
; FILE REFERENCE: TACR2 MMH-0225US  
; CURRENT APPLICATION NUMBER: US/10/160,358  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: PCT/US01/47394  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: 60/247,649  
; PRIOR FILING DATE: 2000-11-09  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-160-358-26

Query Match 53.0%; Score 10.6; DB 8; Length 15;  
Score over Length 70.7%;  
Best Local Similarity 90.9%; Pred. No. 5.9e+05;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGT 14  
DB 4 CCAGTTGAAGT 14  
|||||

RESULT 149  
US-10-138-674-1646/c  
; Sequence 1646, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1646  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-1646

Query Match 60.0%; Score 12; DB 9; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
DB 17 CCCAGTTGAAGT 6  
|||||

RESULT 150  
US-10-138-674-1647/c  
; Sequence 1647, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor



```
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1647
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1647

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 16 CCCAGTTGAAGT 5

RESULT 151
US-10-138-674-6253/c
; Sequence 6253, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6253
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6253

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 15 CCCAGTTGAAGT 4

RESULT 152
US-10-138-674-6254/c
; Sequence 6254, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6254
; LENGTH: 17
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6254

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 12 CCCAGTTGAAGT 1

RESULT 153
US-10-138-674-8571/c
; Sequence 8571, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8571
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8571

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14
Db 14 CCCAGTTGAAGT 3

RESULT 154
US-10-287-949A-1646/c
; Sequence 1646, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1646
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1646

Query Match      60.0%; Score 12; DB 9; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
Db 17 CCCAGTTGAAGT 6

RESULT 155  
US-10-287-949A-1647/C  
; Sequence 1647, Application US/10287949A  
; Publication No. US20040102389A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MEHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; SOFTWARE: PatentIn version 3.0  
; NUMBER OF SEQ ID NOS: 20822  
; SEQ ID NO 1647  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-1647

Query Match 60.0%; Score 12; DB 9; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
Db 16 CCCAGTTGAAGT 5

RESULT 156  
US-10-287-949A-6253/C  
; Sequence 6253, Application US/10287949A  
; Publication No. US20040102389A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MEHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; SOFTWARE: PatentIn version 3.0  
; NUMBER OF SEQ ID NOS: 20822  
; SEQ ID NO 6253  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-6253

Query Match 60.0%; Score 12; DB 9; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
Db 15 CCCAGTTGAAGT 4

## RESULT 157

US-10-287-949A-6254/C  
; Sequence 6254, Application US/10287949A  
; Publication No. US20040102389A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MEHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6254  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-6254

Query Match 60.0%; Score 12; DB 9; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
Db 12 CCCAGTTGAAGT 1

## RESULT 158

US-10-287-949A-8571/C  
; Sequence 8571, Application US/10287949A  
; Publication No. US20040102389A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MEHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8571  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-8571

Query Match 60.0%; Score 12; DB 9; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14  
|||||  
Db 14 CCCAGTTGAAGT 3

## RESULT 159

US-10-712-633-3654/C  
; Sequence 3654, Application US/10712633  
; Publication No. US20040220128A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pamela

```
/ APPLICANT: Sandberg, Jennifer
/ APPLICANT: Gordon, Gilad
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan
/ TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
/ FILE REFERENCE: MBH02-325PCT (400/047)
/ CURRENT APPLICATION NUMBER: US/10/712,633
/ CURRENT FILING DATE: 2003-11-13
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ PRIOR APPLICATION NUMBER: US 09/371,772
/ PRIOR FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 09/708,690
/ PRIOR FILING DATE: 2000-11-07
/ PRIOR APPLICATION NUMBER: US 09/870,161
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: US 60/334,461
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 10/138,674
/ PRIOR FILING DATE: 2002-05-03
/ NUMBER OF SEQ ID NOS: 5989
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3654
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo Sapiens
US-10-712-633-3654

Query Match          60.0%; Score 12; DB 10; Length 17;
Score over Length    70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
DB 14 CCCAGTTGAAGT 3

RESULT 160
US-10-951-303-1646/c
/ Sequence 1646, Application US/10951303
/ Publication No. US20050227937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-K (400/021)
/ CURRENT APPLICATION NUMBER: US/10/951,303
/ CURRENT FILING DATE: 2004-09-27
/ PRIOR APPLICATION NUMBER: US/09/685,664
/ PRIOR FILING DATE: 1995-10-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ PRIOR APPLICATION NUMBER: US 09/371,772
/ PRIOR FILING DATE: 1999-08-10
/ NUMBER OF SEQ ID NOS: 8231
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1646
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-10-951-303-1646

Query Match          60.0%; Score 12; DB 11; Length 17;
Score over Length    70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
DB 16 CCCAGTTGAAGT 5

RESULT 162
US-11-088-219-1646/c
/ Sequence 1646, Application US/11088219
/ Publication No. US20070042029A1
/ GENERAL INFORMATION:
/ APPLICANT: Sirna Therapeutics, Inc.
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan
/ TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-Q (400/266)
/ CURRENT APPLICATION NUMBER: US/11/088,219
/ CURRENT FILING DATE: 2005-03-23
/ PRIOR APPLICATION NUMBER: 10/138,674
/ PRIOR FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: 09/870,161
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 09/708,690
/ PRIOR FILING DATE: 2000-11-07
/ PRIOR APPLICATION NUMBER: 09/371,722
/ PRIOR FILING DATE: 1999-08-10
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Query Match

60.0%; Score 12; DB 11; Length 17;

; PRIOR APPLICATION NUMBER: 08/584,040  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1646  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-088-219-1646

Query Match 60.0%; Score 12; DB 23; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14  
||| ||||| |||||  
Db 17 CCCAGTTGAAGT 6

## RESULT 163

US-11-088-219-1647/c  
; Sequence 1647, Application US/11088219  
; Publication No. US20070042029A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or  
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor  
; FILE REFERENCE: MBH00-876-Q (400/266)  
; CURRENT APPLICATION NUMBER: US/11/088,219  
; CURRENT FILING DATE: 2005-03-23  
; PRIOR APPLICATION NUMBER: 10/138,674  
; PRIOR FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: 09/870,161  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 09/708,690  
; PRIOR FILING DATE: 2000-11-07  
; PRIOR APPLICATION NUMBER: 09/371,722  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 08/584,040  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/005,974  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1647  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-088-219-1647

Query Match 60.0%; Score 12; DB 23; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14  
||| ||||| |||||  
Db 16 CCCAGTTGAAGT 5

## RESULT 164

US-11-088-219-6253/c  
; Sequence 6253, Application US/11088219  
; Publication No. US20070042029A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or  
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor  
; FILE REFERENCE: MBH00-876-Q (400/266)  
; CURRENT APPLICATION NUMBER: US/11/088,219  
; CURRENT FILING DATE: 2005-03-23  
; PRIOR APPLICATION NUMBER: 10/138,674  
; PRIOR FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: 09/870,161  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 09/708,690  
; PRIOR FILING DATE: 2000-11-07  
; PRIOR APPLICATION NUMBER: 09/371,722  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 08/584,040  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6253  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-088-219-6253

Query Match 60.0%; Score 12; DB 23; Length 17;  
Score over Length 70.6%;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAAGT 14  
||| ||||| |||||  
Db 15 CCCAGTTGAAGT 4

## RESULT 165

US-11-088-219-6254/c  
; Sequence 6254, Application US/11088219  
; Publication No. US20070042029A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or  
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor  
; FILE REFERENCE: MBH00-876-Q (400/266)  
; CURRENT APPLICATION NUMBER: US/11/088,219  
; CURRENT FILING DATE: 2005-03-23  
; PRIOR APPLICATION NUMBER: 10/138,674  
; PRIOR FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: 09/870,161  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 09/708,690  
; PRIOR FILING DATE: 2000-11-07  
; PRIOR APPLICATION NUMBER: 09/371,722  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 08/584,040  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6254  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-088-219-6254

```
Query Match      60.0%; Score 12; DB 23; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
   |||||
Db 12 CCCAGTTGAAGT 1

RESULT 166
US-11-088-219-8571/c
; Sequence 8571, Application US/11088219
; Publication No. US20070042029A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Enzymatic Nucleic Acid-Mediated Treatment of Ocular Diseases or
; TITLE OF INVENTION: Conditions Related to Levels of Vascular Endothelial Growth Factor
; TITLE OF INVENTION: (VEGF-R)
; FILE REFERENCE: MBHB00-876-Q (400/266)
; CURRENT APPLICATION NUMBER: US/11/088,219
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 10/138,674
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/371,722
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 08/584,040
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/005,974
; PRIOR FILING DATE: 1995-10-26
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8571
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-088-219-8571

Query Match      60.0%; Score 12; DB 23; Length 17;
Score over Length 70.6%;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCCAGTTGAAGT 14
   |||||
Db 14 CCCAGTTGAAGT 3

RESULT 167
US-10-310-914A-1191074/c
; Sequence 1191074, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1191074
; LENGTH: 19
; TYPE: RNA
```

```
; ORGANISM: Human
US-10-310-914A-1191074

Query Match      67.0%; Score 13.4; DB 12; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGTTGAAGTTGCC 18
   |||||
Db 17 CCAGTTGAAGTTGCC 3

RESULT 168
US-10-714-333A-726378/c
; Sequence 726378, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726378
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-726378

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 17 AGTTGAAGTTGCCGT 3

RESULT 169
US-10-714-333A-726385/c
; Sequence 726385, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726385
; LENGTH: 19
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-726385

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 18 AGTTGAAGTTGCCGT 4

RESULT 170
US-10-714-333A-1192689/c
; Sequence 1192689, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192689
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1192689

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 16 AGTTGAAGTTGCCGT 2

RESULT 171
US-10-714-333A-1192696/c
; Sequence 1192696, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192696

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1192696

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 18 AGTTGAAGTTGCCGT 4

RESULT 172
US-10-714-333A-1192704/c
; Sequence 1192704, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192704
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1192704

Query Match      67.0%; Score 13.4; DB 15; Length 19;
Score over Length 70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
   |||||
Db 18 AGTTGAAGTTGCCGT 4

RESULT 173
US-11-083-784-726378/c
; Sequence 726378, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
```

```
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726378
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-726378

Query Match          67.0%; Score 13.4; DB 19; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
Db 17 AGTTGAAGTTGCCCT 3

RESULT 174
US-11-083-784-726385/c
; Sequence 726385, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726385
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-726385

Query Match          67.0%; Score 13.4; DB 19; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
Db 17 AGTTGAAGTTGCCCT 3

RESULT 175
US-11-083-784-1192689/c
; Sequence 1192689, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192689
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1192689

Query Match          67.0%; Score 13.4; DB 19; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
Db 17 AGTTGAAGTTGCCCT 3

RESULT 176
US-11-083-784-1192696/c
; Sequence 1192696, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192696
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1192696

Query Match          67.0%; Score 13.4; DB 19; Length 19;
Score over Length    70.5%;
Best Local Similarity 93.3%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20
Db 17 AGTTGAAGTTGCCCT 3

RESULT 177
US-11-083-784-1192704/c
; Sequence 1192704, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1192704
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1192704
```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784

; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333

; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 1192704

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-083-784-1192704

Query Match 67.0%; Score 13.4; DB 19; Length 19;

Score over Length 70.5%;

Best Local Similarity 93.3%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20

|||||

Db 18 AGTTGAAGTTGCCGT 4

RESULT 178

US-11-101-244-726378/c

; Sequence 726378, Application US/11/101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244

; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 726378

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-101-244-726378

Query Match 67.0%; Score 13.4; DB 20; Length 19;

Score over Length 70.5%;

Best Local Similarity 93.3%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20

|||||

Db 17 AGTTGAAGTTGCCGT 3

RESULT 179

US-11-101-244-726385/c

; Sequence 726385, Application US/11/101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244

; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 726385

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-101-244-726385

Query Match 67.0%; Score 13.4; DB 20; Length 19;

Score over Length 70.5%;

Best Local Similarity 93.3%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20

|||||

Db 18 AGTTGAAGTTGCCGT 4

RESULT 180

US-11-101-244-1192689/c

; Sequence 1192689, Application US/11/101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244

; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 1192689

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-101-244-1192689

Query Match 67.0%; Score 13.4; DB 20; Length 19;

Score over Length 70.5%;

Best Local Similarity 93.3%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTTGCCGT 20

|||||

Db 16 AGTTGAAGTTGCCGT 2

RESULT 181

US-11-101-244-1192696/c

; Sequence 1192696, Application US/11/101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia



; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1192696  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1192696

Query Match 67.0%; Score 13.4; DB 20; Length 19;  
Score over Length 70.5%;  
Best Local Similarity 93.3%; Pred. No. 2.2e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTGGCGT 20  
|||||  
DB 17 AGTTGAAGTGGCGT 3

## RESULT 182

US-11-101-244-1192704/c  
; Sequence 1192704, Application US/11/101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1192704  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1192704

Query Match 67.0%; Score 13.4; DB 20; Length 19;  
Score over Length 70.5%;  
Best Local Similarity 93.3%; Pred. No. 2.2e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTGGCGT 20  
|||||  
DB 18 AGTTGAAGTGGCGT 4

## RESULT 183

US-10-535-164-474753  
; Sequence 474753, Application US/10535164  
; Publication No. US20070134655A1  
; GENERAL INFORMATION:  
; APPLICANT: BENTWICH, ITZHAK

; TITLE OF INVENTION: Bioinformatically detectable of Novel Regulatory genes and thereo  
; FILE REFERENCE: 050992.0200.PCUS13  
; CURRENT APPLICATION NUMBER: US/10/535,164  
; CURRENT FILING DATE: 2005-05-16  
; NUMBER OF SEQ ID NOS: 548156  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 474753  
; LENGTH: 16  
; TYPE: RNA  
; ORGANISM: Human  
US-10-535-164-474753

Query Match 56.0%; Score 11.2; DB 17; Length 16;  
Score over Length 70.0%;  
Best Local Similarity 68.8%; Pred. No. 2.9e+05;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCCCAGTTGAAGTTG 16  
|||||  
DB 1 GUCCAGUGGAGCUG 16

## RESULT 184

US-10-078-958-50/c  
; Sequence 50, Application US/10078958  
; Publication No. US20030070185A1  
; GENERAL INFORMATION:  
; APPLICANT: JAKOBOVITS, AYA  
; APPLICANT: KUCHERLAPATI, RAJU  
; APPLICANT: KLAPHOLZ, SUSAN  
; APPLICANT: MENDEZ, MICHAEL J.  
; APPLICANT: GREEN, LARRY  
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING  
; TITLE OF INVENTION: PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED  
; FILE REFERENCE: CELL 4.18 CON  
; CURRENT APPLICATION NUMBER: US/10/078,958  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 08/759,620  
; PRIOR FILING DATE: 1996-12-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-078-958-50

Query Match 42.0%; Score 8.4; DB 7; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCCAGTTG 10  
|||||  
DB 12 GCCCCAGTAG 3

## RESULT 185

US-10-078-958-59/c  
; Sequence 59, Application US/10078958  
; Publication No. US20030070185A1  
; GENERAL INFORMATION:  
; APPLICANT: JAKOBOVITS, AYA  
; APPLICANT: KUCHERLAPATI, RAJU  
; APPLICANT: KLAPHOLZ, SUSAN  
; APPLICANT: MENDEZ, MICHAEL J.  
; APPLICANT: GREEN, LARRY  
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING  
; TITLE OF INVENTION: PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED  
; FILE REFERENCE: CELL 4.18 CON  
; CURRENT APPLICATION NUMBER: US/10/078,958

US-10-535-164-474753  
; Sequence 474753, Application US/10535164  
; Publication No. US20070134655A1  
; GENERAL INFORMATION:  
; APPLICANT: BENTWICH, ITZHAK

; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 08/759,620  
; PRIOR FILING DATE: 1996-12-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 59  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-078-958-59

Query Match 42.0%; Score 8.4; DB 7; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCCCAGTTG 10  
Db 12 GCCCCAGTAG 3

## RESULT 186

US-10-257-017B-269582/c  
; Sequence 269582, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 269582  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001812  
US-10-257-017B-269582

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
Db 10 AGTTGAAGTT 1

## RESULT 187

US-10-257-017B-269967/c  
; Sequence 269967, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 269967  
; LENGTH: 12

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001948  
US-10-257-017B-269967

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
Db 11 AGTTGAAGAT 2

## RESULT 188

US-10-257-017B-270364/c  
; Sequence 270364, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 270364  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002104  
US-10-257-017B-270364

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
Db 10 AGTTGAATTT 1

## RESULT 189

US-10-257-017B-270867/c  
; Sequence 270867, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 270867  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002305  
US-10-257-017B-270867

```
Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTTGAATTT 1

RESULT 190
US-10-257-017B-272438
; Sequence 272438, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 272438
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002817
US-10-257-017B-272438

Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 3 AGTTGAATTT 12

RESULT 191
US-10-257-017B-272556/c
; Sequence 272556, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 272556
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002858
US-10-257-017B-272556

Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTT 15
DB 11 AGTTAAGTT 2

RESULT 192
US-10-257-017B-274200
; Sequence 274200, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 274200
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003474
US-10-257-017B-274200

Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 3 GTTGAAGTAG 12

RESULT 193
US-10-257-017B-274757/c
; Sequence 274757, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 274757
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003668
US-10-257-017B-274757

Query Match          42.0%; Score 8.4; DB 10; Length 12;
Score over Length    70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTCGAAGTT 1
```

```
RESULT 194
US-10-257-017B-280041/c
; Sequence 280041, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 280041
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008088
US-10-257-017B-280041

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      10 AGTTGAAGTT 1

RESULT 195
US-10-257-017B-281065
; Sequence 281065, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281065
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009391
US-10-257-017B-281065

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTG 16
Db      2 GTAGAAGTTG 11

RESULT 196
US-10-257-017B-281930/c
; Sequence 281930, Application US/10257017B
; Publication No. US20040241651A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 281930
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010165
US-10-257-017B-281930

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTG 16
Db      11 GTTGAAGTTG 2

RESULT 197
US-10-257-017B-284490
; Sequence 284490, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 284490
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011855
US-10-257-017B-284490

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      2 AGTGAAGTT 11

RESULT 198
US-10-257-017B-285659
; Sequence 285659, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 285659
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012392
US-10-257-017B-285659

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      1 AGTTGAAGTT 10

RESULT 199
US-10-257-017B-286867/c
; Sequence 286867, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 286867
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012861
US-10-257-017B-286867

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      12 AGTTGAAGTT 3

RESULT 200
US-10-257-017B-288407/c
; Sequence 288407, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 288407
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013497
US-10-257-017B-288407

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      12 GTTGAAGTTG 3

RESULT 201
US-10-257-017B-290224/c
; Sequence 290224, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290224
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014248
US-10-257-017B-290224

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTTGAAGTT 1

RESULT 202
US-10-257-017B-292655/c
; Sequence 292655, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 292655
; LENGTH: 12
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015296
US-10-257-017B-292655

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      12 AGTTGAAGTT 3

RESULT 203
US-10-257-017B-292658/c
; Sequence 292658, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 292658
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015297
US-10-257-017B-292658

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      11 AGTTGAAGAT 2

RESULT 204
US-10-257-017B-292707/c
; Sequence 292707, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 292707
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015313
US-10-257-017B-292707
```

```

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTTGAAGTT 1

RESULT 205
US-10-257-017B-293121/c
; Sequence 293121, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 293121
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015507
US-10-257-017B-293121

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      12 AGTTGAAGTT 3

RESULT 206
US-10-257-017B-293477/c
; Sequence 293477, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 293477
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015632
US-10-257-017B-293477

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      6 AGTTGAAGTT 15
      |||||
Db     11 AGTTGAAGCT 2

RESULT 207
US-10-257-017B-293667/c
; Sequence 293667, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 293667
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015722
US-10-257-017B-293667

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
      |||||
Db     11 AGTTGAAGTT 2

RESULT 208
US-10-257-017B-294586/c
; Sequence 294586, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 294586
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016192
US-10-257-017B-294586

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
      |||||
Db     11 AGTTGAAGTT 2

RESULT 209
US-10-257-017B-295090
; Sequence 295090, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295090
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016430
US-10-257-017B-295090

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
      . |||| |
Db     2 GTTGAAGTTG 11

RESULT 210
US-10-257-017B-295284
; Sequence 295284, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295284
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016521
US-10-257-017B-295284

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
      |||||
Db     3 AGTTGAAGTT 12

RESULT 211
US-10-257-017B-296295/c
; Sequence 296295, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
```

; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 296295  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017012  
US-10-257-017B-296295

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
||| |||||  
Db 12 AGTAGAAGTT 3

RESULT 212  
US-10-257-017B-296487  
; Sequence 296487, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 296487  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017101  
US-10-257-017B-296487

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
||| |||||  
Db 3 AGTAGAAGTT 12

RESULT 213  
US-10-257-017B-297323  
; Sequence 297323, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07

; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 297323  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017523  
US-10-257-017B-297323

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
||| |||||  
Db 2 AGTTGAGTT 11

RESULT 214  
US-10-257-017B-298042  
; Sequence 298042, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 298042  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017887  
US-10-257-017B-298042

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
||| |||||  
Db 3 GTTGAAGTTG 12

RESULT 215  
US-10-257-017B-299239  
; Sequence 299239, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07



```
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 299239
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018492
US-10-257-017B-299239

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 3 ATTTGAAGTT 12

RESULT 216
US-10-257-017B-300438
/ Sequence 300438, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 300438
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019035
US-10-257-017B-300438

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 3 GTTAAAGTTG 12

RESULT 217
US-10-257-017B-302312
/ Sequence 302312, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 302312
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019928
US-10-257-017B-302312

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11

RESULT 218
US-10-257-017B-302603/c
/ Sequence 302603, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 302603
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020078
US-10-257-017B-302603

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 10 AGTTTAAAGTT 1

RESULT 219
US-10-257-017B-302958
/ Sequence 302958, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 302958
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020249
US-10-257-017B-302958

Query Match      42.0%; Score 8.4; DB 10; Length 12;
```

```
Score over Length 70.0%; Pred. No. 7.8e+06;
Best Local Similarity 90.0%; 0; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 7 GTTGAAGTTG 16
Db 2 GTTGAAGATG 11

RESULT 220
US-10-257-017B-304877
; Sequence 304877, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 304877
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021148
US-10-257-017B-304877

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11

RESULT 221
US-10-257-017B-306204/C
; Sequence 306204, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306204
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021865
US-10-257-017B-306204

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11

RESULT 222
US-10-257-017B-306498
; Sequence 306498, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306498
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022053
US-10-257-017B-306498

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 2 AGTTGAAGTT 11

RESULT 223
US-10-257-017B-306928
; Sequence 306928, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306928
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022250
US-10-257-017B-306928

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15
Db 3 AGTTGAAGTT 12

RESULT 224
```

```
US-10-257-017B-309177
; Sequence 309177, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 309177
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023399
US-10-257-017B-309177

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 3 AGTTGAAGTT 12

RESULT 225
US-10-257-017B-310209
; Sequence 310209, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310209
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023863
US-10-257-017B-310209

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 1 GTTGAAGTTG 10

RESULT 226
US-10-257-017B-310210
; Sequence 310210, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 310210
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023863
US-10-257-017B-310210

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 1 GTTGAAGTTG 10

RESULT 227
US-10-257-017B-312793
; Sequence 312793, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 312793
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025301
US-10-257-017B-312793

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 2 GTTGAAGTTG 11

RESULT 228
US-10-257-017B-316105/C
; Sequence 316105, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 316105
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027285
US-10-257-017B-316105
```

```
Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTT 15
Db 10 AGTTAAAGTT 1
```

## RESULT 229

```
US-10-257-017B-316407
; Sequence 316407, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 316407
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027431
US-10-257-017B-316407
```

```
Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 GTTGAAGTTG 16
Db 1 GTTGAATTG 10
```

## RESULT 230

```
US-10-257-017B-316595/c
; Sequence 316595, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 316595
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027519
US-10-257-017B-316595
```

```
Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 GTTGAAGTTG 16
Db 11 GTTGAATTG 2
```

## RESULT 231

```
US-10-257-017B-316596/c
; Sequence 316596, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 316596
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027519
US-10-257-017B-316596
```

```
Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 GTTGAAGTTG 16
Db 11 GTTGAATTG 2
```

## RESULT 232

```
US-10-257-017B-317245/c
; Sequence 317245, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317245
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027885  
US-10-257-017B-317245

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
| | | | | | | | | | | | | |  
Db 12 AATTGAAGTT 3

## RESULT 233

US-10-257-017B-317868/c  
; Sequence 317868, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 317868  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028311  
US-10-257-017B-317868

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
| | | | | | | | | | | | | |  
Db 11 AATTGAAGTT 2

## RESULT 234

US-10-257-017B-317906/c  
; Sequence 317906, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 317906  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide-Primer  
US-10-257-017B-317906

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
| | | | | | | | | | | | | |  
Db 12 AATTGAAGTT 3

## RESULT 235

US-10-257-017B-318475/c  
; Sequence 318475, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 318475  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028677  
US-10-257-017B-318475

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
| | | | | | | | | | | | | |  
Db 10 AATTGAAGTT 1

## RESULT 236

US-10-257-017B-321495/c  
; Sequence 321495, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 321495  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030284  
US-10-257-017B-321495

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
| | | | | | | | | | | | | |

```
Db      12 GTTGAAGTGG 3

RESULT 237
US-10-257-017B-322078/c
; Sequence 322078, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322078
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030647
US-10-257-017B-322078

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      10 AGTTGAGTT 1

RESULT 238
US-10-257-017B-323774/c
; Sequence 323774, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323774
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031607
US-10-257-017B-323774

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      12 ATTTGAAGTT 3

RESULT 239
US-10-257-017B-323855/c
```

```
; Sequence 323855, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323855
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031647
US-10-257-017B-323855

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GTTGAAGTTG 16
Db      12 GTTGAAGTTG 3

RESULT 240
US-10-257-017B-327363/c
; Sequence 327363, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 327363
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033594
US-10-257-017B-327363

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 AGTTGAAGTT 15
Db      11 AGTTTAAAGTT 2

RESULT 241
US-10-257-017B-328966/c
; Sequence 328966, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 328966
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034675
US-10-257-017B-328966

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      11 GTTAAAGTTG 2

RESULT 242
US-10-257-017B-329138/c
; Sequence 329138, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329138
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034774
US-10-257-017B-329138

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTTGAATT 1

RESULT 243
US-10-257-017B-329589
; Sequence 329589, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331303
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0035020
US-10-257-017B-329589

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTTGAATT 1

RESULT 244
US-10-257-017B-329753
; Sequence 329753, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329753
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0035126
US-10-257-017B-329753

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      3 GTTGAATTG 12

RESULT 245
US-10-257-017B-331303/c
; Sequence 331303, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331303
```

```

; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036110
US-10-257-017B-331303

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GTTGAGGTTG 3

RESULT 246
US-10-257-017B-331432/c
; Sequence 331432, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331432
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036202
US-10-257-017B-331432

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GTTGAGGTTG 3

RESULT 247
US-10-257-017B-331579/c
; Sequence 331579, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331579
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036328

```

US-10-257-017B-331579

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
Db 11 AGTTGAGTT 2

RESULT 248

US-10-257-017B-331707/c  
; Sequence 331707, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 331707  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide-Primer  
US-10-257-017B-331707

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
Db 11 AGTTGAGTT 2

RESULT 249

US-10-257-017B-332215/c  
; Sequence 332215, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 332215  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036773  
US-10-257-017B-332215

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;



Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 11 AGTTGAAGTT 2

## RESULT 250

US-10-257-017B-333855/c  
; Sequence 333855, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 333855  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037792  
US-10-257-017B-333855

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 11 AGTTGAAGTT 2

## RESULT 251

US-10-257-017B-333880  
; Sequence 333880, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 333880  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037804  
US-10-257-017B-333880

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 3 AGTTGAAGTT 12

## RESULT 252

US-10-257-017B-336184/c  
; Sequence 336184, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 336184  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039238  
US-10-257-017B-336184

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
|||||  
Db 12 GTTGAAGTTG 3

## RESULT 253

US-10-257-017B-338774/c  
; Sequence 338774, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 338774  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040669  
US-10-257-017B-338774

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 10 AGTTGAAGTT 1

## RESULT 254

US-10-257-017B-338942  
; Sequence 338942, Application US/10257017B

```
Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338942
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040756
US-10-257-017B-338942

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 1 GTTGAAGTAG 10

RESULT 255
US-10-257-017B-339290
; Sequence 339290, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 339290
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007278
US-10-257-017B-339290

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 2 AGTTGAATTT 11

RESULT 256
US-10-017B-341683
; Sequence 341683, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
```

```
Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341683
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042183
US-10-257-017B-341683

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 2 GTTGAAGTTG 11

RESULT 257
US-10-257-017B-341694/c
; Sequence 341694, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341694
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042185
US-10-257-017B-341694

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 10 GTTGAAGTTG 1

RESULT 258
US-10-257-017B-341790/c
; Sequence 341790, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
```

; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 341790  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042229  
US-10-257-017B-341790

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16  
Db 12 GTTAAAGTTG 3

RESULT 259  
US-10-257-017B-342185/c  
; Sequence 342185, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 342185  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042419  
US-10-257-017B-342185

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
Db 11 AGTTAAAGTT 2

RESULT 260  
US-10-257-017B-343124  
; Sequence 343124, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 343124  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043488  
US-10-257-017B-344303

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042902  
US-10-257-017B-343124

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
Db 2 AGTTAAAGTT 11

RESULT 261

US-10-257-017B-343306  
; Sequence 343306, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 343306  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010454  
US-10-257-017B-343306

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16  
Db 3 GTTTAAGTTG 12

RESULT 262

US-10-257-017B-344303  
; Sequence 344303, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 344303  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043488  
US-10-257-017B-344303

```
Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
      ||||| |||||
Db      2 AGTTTAAAGTT 11

RESULT 263
US-10-257-017B-346809
; Sequence 346809, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 346809
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044779
US-10-257-017B-346809

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
      ||||| |||||
Db      2 AGTTGAAGAT 11

RESULT 264
US-10-257-017B-347105/c
; Sequence 347105, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 347105
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044912
US-10-257-017B-347105

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      6 AGTTGAAGTT 15
      ||||| |||||
Db      11 AGTTAAAGTT 2

RESULT 265
US-10-257-017B-347106/c
; Sequence 347106, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 347106
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044912
US-10-257-017B-347106

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
      ||||| |||||
Db      11 AGTTAAAGTT 2

RESULT 266
US-10-257-017B-347275
; Sequence 347275, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 347275
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045008
US-10-257-017B-347275

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
      ||||| |||||
Db      2 AGTTAAAGTT 11
```

```
RESULT 267
US-10-257-017B-347597/c
; Sequence 347597, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 347597
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045181
US-10-257-017B-347597

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      11 GTTGAATTG 2

RESULT 268
US-10-257-017B-348478/c
; Sequence 348478, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 348478
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045610
US-10-257-017B-348478

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      11 ATTTCAGTT 2

RESULT 269
US-10-257-017B-352722
; Sequence 352722, Application US/10257017B
; Publication No. US20040241651A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 352722
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048058
US-10-257-017B-352722
```

```
Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GTTGAAGTTG 16
Db      2 GTTTAAGTTG 11
```

```
RESULT 270
US-10-257-017B-352762/c
; Sequence 352762, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 352762
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048084
US-10-257-017B-352762
```

```
Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGTTGAAGTT 15
Db      10 AGTTGTAGTT 1
```

```
RESULT 271
US-10-257-017B-352880/c
; Sequence 352880, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

;; TITLE OF INVENTION: methylations  
;; FILE REFERENCE: E01/1193/WO  
;; CURRENT APPLICATION NUMBER: US/10/257,017B  
;; PRIOR FILING DATE: 2002-10-07  
;; PRIOR APPLICATION NUMBER: DE 10019173.8  
;; PRIOR FILING DATE: 2000-04-07  
;; NUMBER OF SEQ ID NOS: 382046  
;; SEQ ID NO 352880  
;; LENGTH: 12  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048150  
US-10-257-017B-352880

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 12 AGTTGAGTT 3

## RESULT 272

US-10-257-017B-353886/c  
;; Sequence 353886, Application US/10257017B  
;; Publication No. US20040241651A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Alexander Olek  
;; APPLICANT: Christian Piepenbrock  
;; APPLICANT: Kurt Berlin  
;; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
;; FILE REFERENCE: E01/1193/WO  
;; CURRENT APPLICATION NUMBER: US/10/257,017B  
;; CURRENT FILING DATE: 2002-10-07  
;; PRIOR APPLICATION NUMBER: DE 10019173.8  
;; PRIOR FILING DATE: 2000-04-07  
;; NUMBER OF SEQ ID NOS: 382046  
;; SEQ ID NO 353886  
;; LENGTH: 12  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048785  
US-10-257-017B-353886

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 12 AGTTGAAGT 3

## RESULT 273

US-10-257-017B-354932  
;; Sequence 354932, Application US/10257017B  
;; Publication No. US20040241651A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Alexander Olek  
;; APPLICANT: Christian Piepenbrock  
;; APPLICANT: Kurt Berlin  
;; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
;; FILE REFERENCE: E01/1193/WO  
;; CURRENT APPLICATION NUMBER: US/10/257,017B  
;; CURRENT FILING DATE: 2002-10-07  
;; PRIOR APPLICATION NUMBER: DE 10019173.8

;; PRIOR FILING DATE: 2000-04-07  
;; NUMBER OF SEQ ID NOS: 382046  
;; SEQ ID NO 354932  
;; LENGTH: 12  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010418  
US-10-257-017B-354932

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16  
|||||  
Db 1 GTTGAAGTGG 10

## RESULT 274

US-10-257-017B-355010  
;; Sequence 355010, Application US/10257017B  
;; Publication No. US20040241651A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Alexander Olek  
;; APPLICANT: Christian Piepenbrock  
;; APPLICANT: Kurt Berlin  
;; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
;; FILE REFERENCE: E01/1193/WO  
;; CURRENT APPLICATION NUMBER: US/10/257,017B  
;; CURRENT FILING DATE: 2002-10-07  
;; PRIOR APPLICATION NUMBER: DE 10019173.8  
;; PRIOR FILING DATE: 2000-04-07  
;; NUMBER OF SEQ ID NOS: 382046  
;; SEQ ID NO 355010  
;; LENGTH: 12  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049419  
US-10-257-017B-355010

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
|||||  
Db 3 AATTGAAGTT 12

## RESULT 275

US-10-257-017B-355310/c  
;; Sequence 355310, Application US/10257017B  
;; Publication No. US20040241651A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Alexander Olek  
;; APPLICANT: Christian Piepenbrock  
;; APPLICANT: Kurt Berlin  
;; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
;; FILE REFERENCE: E01/1193/WO  
;; CURRENT APPLICATION NUMBER: US/10/257,017B  
;; CURRENT FILING DATE: 2002-10-07  
;; PRIOR APPLICATION NUMBER: DE 10019173.8  
;; PRIOR FILING DATE: 2000-04-07  
;; NUMBER OF SEQ ID NOS: 382046  
;; SEQ ID NO 355310  
;; LENGTH: 12  
;; TYPE: DNA

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049589
US-10-257-017B-355310

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 11 GTTGAGTTG 2

RESULT 276
US-10-257-017B-358202
; Sequence 358202, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358202
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050991
US-10-257-017B-358202

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 3 AGTTGAAGAT 12

RESULT 277
US-10-257-017B-359017/c
; Sequence 359017, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359017
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051425
US-10-257-017B-359017
```

```

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTTGAGTT 2

RESULT 278
US-10-257-017B-359643
; Sequence 359643, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359643
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051694
US-10-257-017B-359643

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 1 AGTTGAGTT 10

RESULT 279
US-10-257-017B-361463
; Sequence 361463, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 361463
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052647
US-10-257-017B-361463

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 6 AGTTGAAGTT 15  
DB 3 AGTTGAAGTT 12

## RESULT 280

US-10-257-017B-361738/c  
; Sequence 361738, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 361738  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052802  
US-10-257-017B-361738

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 11 AGTTGAAGTT 2

## RESULT 281

US-10-257-017B-361979/c  
; Sequence 361979, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 361979  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052975  
US-10-257-017B-361979

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 12 AGTTGAAGTT 3

## RESULT 282

US-10-257-017B-362769/c  
; Sequence 362769, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 362769  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053437  
US-10-257-017B-362769

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 10 AGATGAAGTT 1

## RESULT 283

US-10-257-017B-363267  
; Sequence 363267, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 363267  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053740  
US-10-257-017B-363267

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15  
DB 2 AATTGAAGTT 11

## RESULT 284

US-10-257-017B-363675  
; Sequence 363675, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:



```

; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 363675
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053997
US-10-257-017B-363675

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 AAGTTGCCGT 20
Db 3 AAGTTGTCCT 12

RESULT 285
US-10-257-017B-364075
; Sequence 364075, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 364075
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0054253
US-10-257-017B-364075

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 1 AGTTGAGTT 10

RESULT 286
US-10-257-017B-364597/c
; Sequence 364597, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations

```

```

; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 364597
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0054603
US-10-257-017B-364597

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GATGAAGTTG 3

RESULT 287
US-10-257-017B-366105/c
; Sequence 366105, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 366105
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010825
US-10-257-017B-366105

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
Db 11 AGTGAAGTT 2

RESULT 288
US-10-257-017B-366773/c
; Sequence 366773, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07

```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 366773
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0055962
US-10-257-017B-366773

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 10 GTTGAAGTTG 1

RESULT 289
US-10-257-017B-366978/c
; Sequence 366978, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 366978
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0056077
US-10-257-017B-366978

Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
Db 12 GTTGAAGTTG 3

RESULT 290
US-10-257-017B-367247
; Sequence 367247, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 367247
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0056243
US-10-257-017B-367247
```

```
Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTT 15
Db 1 AGTTAAAGTT 10
```

## RESULT 291

```
US-10-257-017B-367323/c
; Sequence 367323, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 367323
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009154
US-10-257-017B-367323
```

```
Query Match      42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 AGTTGAAGTT 15
Db 10 AGTTAAAGTT 1
```

## RESULT 292

```
US-10-257-017B-369030
; Sequence 369030, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369030
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057415
US-10-257-017B-369030
```

```
Query Match      42.0%; Score 8.4; DB 10; Length 12;
```

```
Score over Length 70.0%; Pred. No. 7.8e+06;
Best Local Similarity 90.0%; 0; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 7 GTTGAAGTTG 16
DB 2 GGTGAAGTTG 11

RESULT 293
US-10-257-017B-369031
; Sequence 369031, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369031
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057415
US-10-257-017B-369031

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 2 GGTGAAGTTG 11

RESULT 294
US-10-257-017B-369870
; Sequence 369870, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369870
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057857
US-10-257-017B-369870

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
```

```
Db 1 AGTTGAAGTT 10

RESULT 295
US-10-257-017B-371399
; Sequence 371399, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 371399
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0058753
US-10-257-017B-371399

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 1 AGTTGAAGTT 10

RESULT 296
US-10-257-017B-371986
; Sequence 371986, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 371986
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0059100
US-10-257-017B-371986

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 1 AGTTGAAGTT 10

RESULT 297
```

```
US-10-257-017B-373586
; Sequence 373586, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 373586
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060183
US-10-257-017B-373586

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 1 AGTTGTAGTT 10

RESULT 298
US-10-257-017B-374860
; Sequence 374860, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 374860
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060940
US-10-257-017B-374860

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GTTGAAGTTG 16
DB 2 GTTGAATTG 11

RESULT 299
US-10-257-017B-375464/c
; Sequence 375464, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 375464
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061264
US-10-257-017B-375464

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 10 AGTGGAGTT 1

RESULT 300
US-10-257-017B-375689
; Sequence 375689, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 375689
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0000447
US-10-257-017B-375689

Query Match 42.0%; Score 8.4; DB 10; Length 12;
Score over Length 70.0%;
Best Local Similarity 90.0%; Pred. No. 7.8e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGTTGAAGTT 15
DB 2 ATTTCAGTT 11

RESULT 301
US-10-257-017B-375855/c
; Sequence 375855, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
```

; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 375855  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061481  
US-10-257-017B-375855

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
||| |||||  
Db 10 AGTTGAAGTT 1

## RESULT 302

US-10-257-017B-376089  
; Sequence 376089, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 376089  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061604  
US-10-257-017B-376089

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTGAAGTTG 16  
||| |||||  
Db 1 GTTGAAGTTG 10

## RESULT 303

US-10-257-017B-376898/c  
; Sequence 376898, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 376898  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0062033  
US-10-257-017B-376898

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
||| |||||  
Db 11 AGTTGAAGTT 2

## RESULT 304

US-10-257-017B-377382/c  
; Sequence 377382, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 377382  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0062298  
US-10-257-017B-377382

Query Match 42.0%; Score 8.4; DB 10; Length 12;  
Score over Length 70.0%;  
Best Local Similarity 90.0%; Pred. No. 7.8e+06;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15  
||| |||||  
Db 11 AATTGAAGTT 2

## RESULT 305

US-10-257-017B-379629/c  
; Sequence 379629, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 379629  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063392  
US-10-257-017B-379629

Query Match 42.0%; Score 8.4; DB 10; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 7.8e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15

|||||

Db 10 AGTTGAAGTT 1

RESULT 306

US-10-257-017B-380089

; Sequence 380089, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; FILE REFERENCE: E01/1193/NO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; PRIOR FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 380089

; LENGTH: 12

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063628

US-10-257-017B-380089

Query Match 42.0%; Score 8.4; DB 10; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 7.8e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGTTGAAGTT 15

|||||

Db 1 AGTTGAAGTT 10

RESULT 307

US-10-708-951-20463/c

; Sequence 20463, Application US/10708951

; Publication No. US20070042982A1

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL

; FILE REFERENCE: 55034

; CURRENT APPLICATION NUMBER: US/10/708,951

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 59824

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 20463

; LENGTH: 12

; TYPE: RNA

; ORGANISM: Homo sapiens

; US-10-708-951-20463

Query Match 42.0%; Score 8.4; DB 16; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 7.8e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 12

|||||

Db 12 CCCAGTTGTA 3

RESULT 308

US-10-708-951-46965/c

; Sequence 46965, Application US/10708951

; Publication No. US20070042982A1

; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL

; FILE REFERENCE: 55034

; CURRENT APPLICATION NUMBER: US/10/708,951

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 59824

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 46965

; LENGTH: 12

; TYPE: RNA

; ORGANISM: Homo sapiens

; US-10-708-951-46965

Query Match 42.0%; Score 8.4; DB 16; Length 12;

Score over Length 70.0%;

Best Local Similarity 90.0%; Pred. No. 7.8e+06;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCAGTTGAA 12

|||||

Db 12 CCCAGTTGTA 3

Search completed: December 3, 2007, 18:13:57

Job time : 1307 secs